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OM protein - protein search, using sw model

Run on: November 14, 2000, 11:54:42 ; Search time 15:21 seconds
(without alignments)
20.233 Million cell updates/sec

Title: US-09-277-074-10
Sequence: 1 KIFGLAFL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_36:*

1: /SIDS1/gcgdata/geneseq/geneseq/AA1980.DAT:*

2: /SIDS1/gcgdata/geneseq/geneseq/AA1981.DAT:*

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13: /SIDS1/gcgdata/geneseq/geneseq/AA1992.DAT:*

14: /SIDS1/gcgdata/geneseq/geneseq/AA1993.DAT:*

15: /SIDS1/gcgdata/geneseq/geneseq/AA1994.DAT:*

16: /SIDS1/gcgdata/geneseq/geneseq/AA1995.DAT:*

17: /SIDS1/gcgdata/geneseq/geneseq/AA1996.DAT:*

18: /SIDS1/gcgdata/geneseq/geneseq/AA1997.DAT:*

19: /SIDS1/gcgdata/geneseq/geneseq/AA1998.DAT:*

20: /SIDS1/gcgdata/geneseq/geneseq/AA1999.DAT:*

21: /SIDS1/gcgdata/geneseq/geneseq/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	100.0	9	15 R73685	Antigen fragment 1
2	43	100.0	9	17 R97507	Cytotoxic T lympho
3	43	100.0	9	18 W36824	Immunogenic peptid
4	43	100.0	9	19 W77131	HER-2/neu syntheti
5	43	100.0	9	19 W78859	HER-1/neu protein
6	43	100.0	9	19 W70057	HER-2/neu derived
7	43	100.0	9	20 Y10495	HLA Class I motif
8	43	100.0	15	21 Y98846	HLA class II bindi
9	43	100.0	624	11 R08222	Extracellular port
10	43	100.0	782	18 W19764	Her2-GM-CSF immuno
11	43	100.0	951	21 Y44993	DC8scfv-erbB2EC fu
12	43	100.0	1255	17 W01111	HER-2/neu protein.

13	43	100.0	1255	20 W92406	Human HER-2/neu on
14	43	100.0	1255	21 Y84780	Amino acid sequenc
15	43	100.0	1255	21 Y92620	Human heregulin 2
16	40	93.0	1433	14 R39568	Sequence of c-erbB
17	32	74.4	932	19 W85040	PK6-green fluorescent
18	32	74.4	933	19 W85039	Green fluorescent
19	31	72.1	28	7 P60883	Synthetic peptide
20	31	72.1	205	21 Y79298	E. coli RhtB prote
21	31	72.1	279	20 Y34701	Amino acid sequenc
22	31	72.1	686	15 R60336	CLC-K1 protein. R
23	31	72.1	687	20 Y13937	Human CLCNKB prote
24	30	69.8	195	18 W00922	HasNPV polypeptide
25	30	69.8	269	15 R48743	G-protein coupled
26	30	69.8	269	17 W02715	G-protein coupled
27	30	69.8	283	21 Y99353	Human PRO1415 (UNQ
28	30	69.8	790	17 R95565	N. meningitidis se
29	30	69.8	790	17 R95568	N. gonorrhoeae B h
30	30	69.8	791	17 R95566	N. meningitidis se
31	30	69.8	792	17 R95567	N. meningitidis se
32	29	67.4	17	21 Y86381	Human gene 16-enco
33	29	67.4	24	16 R65280	M2 region of volta
34	29	67.4	41	19 W75141	Human secreted pro
35	29	67.4	42	19 W75076	Human secreted pro
36	29	67.4	58	20 W67890	Human secreted pro
37	29	67.4	127	18 W36948	Protein encoded by
38	29	67.4	132	21 Y86313	Human secreted pro
39	29	67.4	133	20 W67911	Human secreted pro
40	29	67.4	144	19 W98463	H. pylori GHP0 734
41	29	67.4	186	20 W89879	Antigen 2 from clu
42	29	67.4	296	20 Y34859	C. pneumoniae prot
43	29	67.4	332	18 W20914	H. pylori cytoplas
44	29	67.4	443	21 Y86230	Human secreted pro
45	29	67.4	457	9 P80299	Polygalacturonase.

ALIGNMENTS

RESULT 1

R73685 R73685 standard; peptide: 9 AA.

ID AC R73685;

XX AC R73685;

DT 14-JUN-1995 (first entry)

XX DE Antigen fragment 1, from c-ERB2 has binding affinity for HLA-2.1.

XX KW antigen; epitope; immunogenic target protein; PSA; HBVC; HBVs; EBV;

XX KW HIV1; plasma specific antigen; hepatitis B virus; Epstein Barr;

XX KW human immunodeficiency virus; human papilloma virus; p53; c-ERB2;

XX KW MAGE-1; melanoma antigen-1; core antigen; surface antigen;

XX KW pharmaceutical composition; in vivo; ex vivo; therapeutic;

XX KW diagnostic; MHC class I molecule; major histocompatibility complex;

XX KW HLA-A2.1; 9mer; 10mer; anchor; human leukocyte antigen; PLP; 8mer;

XX KW algorithm prediction; MBP; CMV; cytomagalovirus; HSV;

XX KW herpes simplex virus.

XX OS Homo sapiens.

PN W09420127-A.

PN 15-SEP-1994.

XX PD 04-MAR-1994; 94WO-US02353.

XX PF 05-MAR-1993; 93US-0027146.

XX PR 04-JUN-1993; 93US-0073205.

XX PR 29-NOV-1993; 93US-0159184.

XX (CYTE-) CYTEL CORP.

XX Grey HM, Kast WM, Sette A, Sidney J;

XX WPI; 1994-302678/37.
 XX Immunogenic peptide(s) having an HLA-A2.1 binding motif - used
 PT for treatment or prophylaxis of cancer, virus infection or
 PT autoimmune diseases.
 XX
 XX Disclosure; Page 80; 138pp; English.
 XX
 XX R73685-876 are potential peptide binders of HLA-A2.1 motif. Using
 CC motifs disclosed in the invention, these peptides were screened for
 CC further motifs. Only peptides with binding affinity of at least 1%
 CC (binding affinity is expressed as an IC50 value) as compared to the
 CC standard peptide (R71293) in assays. This peptide has a binding
 CC value of 0.1500. The peptides of the invention can induce cytotoxic
 CC T lymphocytes which can react with target cells. They can be used for
 CC the treatment or prophylaxis of cancer, eg. prostate cancer or
 CC lymphoma, etc.
 XX
 XX Sequence 9 AA;
 SQ

Query Match 100.0%; Score 43; DB 15; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIFGSLAFL 9
 Db 1 kifgslaf1 9
 |||||

RESULT 2
 R97507
 ID R97507 standard; peptide: 9 AA.
 AC
 XX R97507;
 XX
 DT 11-FEB-1997 (first entry)
 DE Cytotoxic T lymphocyte-activating Her-2/Neu-specific peptide.
 XX
 DE p53: Her-2; Neu; aa; amino acid; CTL; cytotoxic T lymphocyte; target;
 KW malignant cell; antigenic; vaccine; immunisation; activation.
 KW
 XX Homo sapiens.
 OS
 XX WO9618409-A1.
 PN
 XX 20-JUN-1996.
 PD
 XX 14-DEC-1995; 95WO-US16415.
 PF
 XX 14-DEC-1994; 94US-0355558.
 PR
 XX (SCRI) SCRIPPS RES INST.
 PA Sherman LA;
 XX WPI; 1996-300385/30.
 XX
 PT In vivo activation of tumour-specific cytotoxic T lymphocytes - by
 PT contacting with polypeptide(s) derived from human p53 or Her-2/Neu
 PT proteins
 PT
 XX Claim 5; Page 124; 158pp; English.
 PS
 XX R97507 is a peptide capable of activating cytotoxic T lymphocytes
 CC (CTLs) which specifically target malignant cells. The peptide
 CC corresponds to amino acids 369-377 of human Her-2/Neu protein. CTL-
 CC activating peptides can be used in a vaccine for protecting against
 CC tumour cell formation. CTLs activated by the peptides will lyse
 CC tumour cells displaying specific peptides. Antibodies against CTL-
 CC activating peptides are useful for the identification of other

CC similar compounds which may be useful for treating cancer or virally-
 CC infected cells, or for diagnosis. The peptide and vaccines produced
 CC provide immunity to a high percentage of different ethnic groups,
 CC i.e. those with different HLA alleles.
 XX
 XX Sequence 9 AA;
 SQ

Query Match 100.0%; Score 43; DB 17; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIFGSLAFL 9
 Db 1 kifgslaf1 9
 |||||

RESULT 3
 W36824
 ID W36824 standard; peptide: 9 AA.
 XX
 AC W36824;
 XX
 DT 23-MAR-1998 (first entry)
 DE Immunogenic peptide H3 based on the human Her-2/neu protein.
 XX
 DE Her-2/neu protein; human leukocyte antigen A2.1; HLA;
 KW cytotoxic T lymphocyte; CTL; immune response; tumour-associated antigen;
 KW T-cell receptor; TCR; tumour treatment.
 KW
 XX Synthetic.
 OS Homo sapiens.
 XX WO9732603-A1.
 PN
 XX 12-SEP-1997.
 PD
 XX 05-MAR-1997; 97WO-US03611.
 PF
 XX 05-MAR-1996; 96US-0012845.
 PR
 XX (SCRI) SCRIPPS RES INST.
 PA Lustgarten J, Sherman LA;
 XX WPI; 1997-470496/43.
 DR
 XX Nucleic acid encoding variable regions of HLA-restricted non-human T
 PT cell receptor specific for tumour antigen - used to identify tumour
 PT antigens and for tumour therapy
 PT
 XX Example 1; Page 9; 34pp; English.
 PS
 XX Synthetic peptides W36824-40 are based on the sequence of the human
 CC Her-2/neu protein, wherein each sequence contains the anchor motif for
 CC human leukocyte antigen (HLA) A2.1. The present peptide is based on
 CC positions 369-377. The ability of these peptides to inhibit the binding
 CC of an influenza virus matrix protein peptide M1 to HLA A2.1 was measured
 CC by inhibition of lysis by an M1 specific, HLA A2.1 restricted, cytotoxic
 CC T lymphocyte (CTL) clone. The present protein showed 38% inhibition. The
 CC peptides were also tested for their ability to elicit an immune response
 CC in vivo. However, only H3 (W36824) and H7 (W36826) were able to do
 CC this. H3 and H7 peptides are tumour-associated antigens, and were used to
 CC immunize a transgenic, non-human vertebrate (that has been modified to
 CC express at least one HLA antigen), so that the animal produces CTL which
 CC displays HLA-restricted T-cell receptor (TCR) specificity for the
 CC antigens. Nucleic acid encoding variable regions of the alpha and beta
 CC chains of such TCRs can be amplified from CTLs produced in the above
 CC manner. Cells expressing recombinant TCR are used to identify antigens
 CC associated with a tumour and to treat tumours in humans. Transgenic mice
 CC are a more convenient source of CTL than the tumour-infiltrating
 CC lymphocytes previously used. TCR can be humanised to reduce

CC side-reactions and short peptide derivatives of TCR are more economical
 CC to produce than TCR itself, particularly when expressed as a
 CC single-chain molecule rather than as a dimer.

XX Sequence 9 AA;

Query Match 100.0%; Score 43; DB 18; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIFGSLAFL 9
 |||||
 Db 1 kifgslaf1 9

RESULT 4

W71131
 ID W71131 standard; peptide; 9 AA.

XX W71131;

XX 16-NOV-1998 (first entry)

XX HER-2/neu synthetic peptide epitope 1.

XX Tyrosinase; tyrosinase cytotoxic lymphocyte response;
 KW cytotoxic T lymphocyte; cysteine-depleted; melanoma.

XX Synthetic.

XX WO9833810-A2.

XX 06-AUG-1998.

XX 29-JAN-1998; 98WO-US01592.

XX 30-JAN-1997; 97US-0037781.

XX (UUVI-) UNIV VIRGINIA PATENT FOUND.

XX Engelhard VH, Hunt DF, Kittlesen D, Slingluff CL;

XX WPI; 1998-437388/37.

XX Disease specific immunogen - comprises disease specific cytotoxic T
 PT lymphocyte epitope used to elicit melanoma specific CTL response

XX Disclosure; Page 27; 93pp; English.

XX The peptide epitope W7119-W7138 were created for human tumour-specific
 CC cytotoxic T lymphocyte response. These peptides are are cysteine-
 CC depleted mutants of a native disease-specific CTL epitope. The cysteine-
 CC depleted CTL epitopes elicit a stronger or more specific CTL response
 CC than the native epitope. The epitopes can be used in a disease-specific
 CC immunogen to protect a mammal against disease in particular melanomas.
 CC The peptides may also be used to screen a sample for the presence of
 CC an antigen with the same epitope, or with a different cross-reactive
 CC epitope.

XX Sequence 9 AA;

Query Match 100.0%; Score 43; DB 19; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIFGSLAFL 9
 |||||
 Db 1 kifgslaf1 9

RESULT 5

W78859

ID W78859 standard; peptide; 9 AA.

XX W78859;

XX 17-NOV-1998 (first entry)

XX HER-1/neu protein fragment 369-377.

XX Microparticle; delivery; polymeric matrix; autoantigen; tumour antigen;
 KW class II associated peptide; pathogen; gene therapy; genetic disease;
 KW infection; downregulation; immune response.

XX Homo sapiens.

XX Synthetic.

XX WO9831398-A1.

XX 23-JUL-1998.

XX 22-JAN-1998; 98WO-US01499.

XX 06-JAN-1998; 98US-0003253.

XX 22-JAN-1997; 97US-0787547.

XX (PANG-) PANGAEA PHARM INC.

XX Curley JM, Hedley ML, Langer RS, Lunsford LB;

XX WPI; 1998-427556/36.

XX New preparations of microparticles - comprising a synthetic polymer
 PT matrix and nucleic acid comprising an expression vector for use in
 PT gene therapy

XX Disclosure; Page 10; 101pp; English.

XX A microparticle preparation (MP) has been developed, consisting of
 CC microparticles having a diameter of less than 100 mu m. The MP comprises:
 CC (a) a polymeric matrix (PM) consisting of one or more synthetic polymers
 CC having a solubility in water of less than 1 mg/l; and (b) an expression
 CC vector selected from RNA molecules (at least 50% of which are closed
 CC circles) or circular plasmid DNA (at least 50% of which are supercoiled).
 CC Also described is a MP of at most 20 microns in diameter, comprising: (a)
 CC a PM; and (b) a NAM comprising an expression control sequence operatively
 CC linked to a coding sequence, where the coding sequence encodes an
 CC expression product selected from: (1) a polypeptide at least 7 amino
 CC acids in length, having a sequence identical to the sequence of: (i) a
 CC fragment of a naturally-occurring mammalian protein; or (ii) a fragment
 CC of a naturally-occurring protein from an infectious agent which infects
 CC a mammal; (2) a peptide having a length and sequence which permits it to
 CC bind to an MHC class I or II molecule; and (3) the polypeptide or the
 CC peptide linked to a trafficking sequence. W69763 to W69765, and W78793
 CC to W78897 are peptide fragments for use in the present invention. The
 CC MPs are highly effective vehicles for the delivery of polynucleotides
 CC into phagocytic cells. They can be used for gene therapy, e.g. for
 CC treating genetic diseases, infections or tumours or for downregulating
 CC an immune response.

XX Sequence 9 AA;

Query Match 100.0%; Score 43; DB 19; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIFGSLAFL 9
 |||||
 Db 1 kifgslaf1 9

RESULT 6

W70057

ID W70057 standard; peptide; 9 AA.
 AC W70057;
 XX
 DT 22-OCT-1998 (first entry)
 XX
 DE HER-2/neu derived HLA-A2.1 binding peptide 5 (residues 369-377).
 XX
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW human leukocyte antigen; HLA; tumour associated antigen; cancer;
 KW antigen presenting cell; APC; immunogenic peptide; immune disorder;
 KW viral infection; AIDS; hepatitis; bacterial infection; malaria;
 KW fungal infection; tuberculosis; melanoma; HER-2/neu; cerB-2.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9833888-A1.
 XX
 PD 06-AUG-1998.
 XX
 PF 30-JAN-1998; 98WO-US01959.
 XX
 PR 31-JAN-1997; 97US-0036696.
 XX
 XX (EPTM-) EPIMMUNE INC.
 PA
 XX
 PI Cellis E, Sette A, Sidney J, Southwood S, Tsai V;
 XX
 DR WPI; 1998-437445/37.
 XX
 XX
 PT Production of antigen-specific cytotoxic T cells - by incubating
 PT immunogenic peptide(s) from antigen that binds class I major
 PT histocompatibility complex molecules with pre-treated antigen
 PT presenting cells
 XX
 PS Example 7; Page 77; 104pp; English.
 XX
 CC Sequences shown in W70053 to W70075 represent peptides derived from
 CC HER-2/neu (cerB-2) antigen. The peptides can bind to a human leukocyte
 CC antigen (HLA), HLA-A2.1 and are used to exemplify the method of
 CC invention of producing antigen-specific cytotoxic T cells (CTLs) in
 CC vitro. The method comprises contacting immunogenic peptides from an
 CC antigen that binds class I major histocompatibility complex (MHC)
 CC molecules with antigen presenting cells (APCs) pretreated with
 CC pretreatment growth factors, and incubating the APCs with purified
 CC cells in the presence of at least 2 incubation growth factors, thereby
 CC producing antigen-specific CTLs. A method for specifically killing
 CC target cells in a human patient is also provided which comprises
 CC obtaining a fluid sample containing CTLs from a patient, contacting the
 CC cytotoxic T cells with APCs pretreated with pre-treatment growth factors,
 CC where the APCs comprise class I MHC molecules. The pretreated APCs are
 CC incubated with the cytotoxic growth factors, thereby producing activated
 CC CTLs which are contacted with a carrier to form a composition. The
 CC composition can then be administered to the patient. The activated CTLs
 CC can be used for treating cancers, immune disorders, viral infections,
 CC AIDS, hepatitis, bacterial infection, fungal infection, malaria or
 CC tuberculosis.
 XX
 SQ Sequence 9 AA;
 Query Match 100.0%; Score 43; DB 19; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIFGSLAFL 9
 DB 1 kifgslaf1 9
 RESULT 7
 Y10495
 ID Y98846 standard; Peptide; 15 AA.
 AC Y98846;
 XX
 DT 07-AUG-2000 (first entry)
 XX
 DE
 XX
 KW Cytotoxic T-lymphocyte response; CTL; antigen; lymphatic system;
 KW immunisation; tumour; infectious disease; immunotherapy; cancer;
 KW malignant melanoma; viral disease; hepatitis; AIDS.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9902183-A2.
 XX
 PD 21-JAN-1999.
 XX
 PF 10-JUL-1998; 98WO-US14289.
 XX
 PR 10-DEC-1997; 97US-0988320.
 XX
 PR 10-JUL-1997; 97CA-2209815.
 XX
 XX (CTLI-) CTL IMMUNOTHERAPIES CORP.
 PA
 XX
 PI Kuendig TM, Simard JJJ;
 XX
 DR WPI; 1999-120514/10.
 XX
 XX Inducing a cytotoxic T lymphocyte response - by maintaining a level
 PT of antigen in the lymphatic system of a mammal so as to provide a
 PT sustained CTL response, used to treat, e.g. AIDS
 XX
 PS Disclosure; Page 43; 199pp; English.
 XX
 CC The present invention describes a method of inducing and/or sustaining
 CC an immunological cytotoxic T lymphocyte (CTL) response in a mammal. The
 CC method comprises: (a) delivering an antigen to the mammal at a level to
 CC induce an immunological CTL response in the mammal; and (b) maintaining
 CC the level of the antigen in the mammal's lymphatic system to maintain
 CC the immunologic CTL response. The method can be used for the delivery of
 CC e.g. a differentiation antigen, a tumour-specific multilignage antigen,
 CC an embryonic antigen, an oncogene antigen, a mutated tumour-suppressor
 CC gene antigen, or a viral antigen. They can be used for the treatment of
 CC disease such as cancer, e.g. malignant melanoma or infectious disease,
 CC e.g. viral disease such as hepatitis or AIDS. Sustained antigen delivery
 CC to the lymphatic system provides for potent CTL stimulation that takes
 CC place in the milieu of the lymphoid organ, and it sustains stimulation
 CC that is necessary to keep CTL active, cytotoxic and recirculating
 CC through the body. Y10071 to Y10639 represent examples of peptide
 CC antigens given in the present invention.
 XX
 SQ Sequence 9 AA;
 Query Match 100.0%; Score 43; DB 20; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIFGSLAFL 9
 DB 1 kifgslaf1 9
 RESULT 8
 Y98846
 ID Y98846 standard; Peptide; 15 AA.
 AC Y98846;
 XX
 DT 07-AUG-2000 (first entry)
 XX

DE HLA class II binding antigen epitope peptide #35.

XX Human leucocyte antigen; HLA class II; antigen epitope; pharmaceutical;
 KW immune response; chronic viral disease; cancer; autoimmune disease;
 KW rheumatoid arthritis; multiple sclerosis; myasthenia gravis; AIDS;
 KW allograft rejection; allergy; Lyme disease; hepatitis; prostate cancer;
 KW glomerulonephritis; food hypersensitivity; malaria.

XX Unidentified.

XX WO9961916-A1.

PN 02-DEC-1999.

XX 28-MAY-1999; 99WO-US12066.

XX 29-MAY-1998; 98US-0087192.

XX (EPIM-) EPIMUNE INC.

XX Sette A, Southwood S, Sidney J;

XX WPI; 2000-097143/08.

XX New compositions containing immunogenic peptide epitopes for various
 PT HLA class II DR molecules useful for inducing helper T cell response -

XX Claim 1; Page 40; 60pp; English.

CC The present invention relates to a new pharmaceutical composition
 CC comprising a unit dose form of a peptide, or analogue, comprising an
 CC epitope selected from those represented by peptides Y9812-Y99339 which
 CC are derived from various antigens for various human leucocyte antigen
 CC class DR molecules, representative of the world wide population. The
 CC peptide/analogue binds to an HLA class II molecule at an IC-50 of less
 CC than or equal to 1,000 nM. The pharmaceutical can be used to induce a
 CC helper T cell response. The pharmaceutical focuses the immune response
 CC towards selected determinants and could therefore be used in cases of
 CC chronic viral diseases and cancer. Examples of diseases that can be
 CC treated using the peptide containing pharmaceutical include autoimmune
 CC diseases (rheumatoid arthritis, multiple sclerosis, and myasthenia
 CC gravis), allograft rejection, allergies, Lyme disease, hepatitis,
 CC post-streptococcal endocarditis or glomerulonephritis and food
 CC hypersensitivities. The peptide epitopes can be used to enhance immune
 CC responses against other immunogens administered with the peptides.
 CC Diseases which can be treated using immunogenic mixtures include prostate
 CC cancer, hepatitis B, hepatitis C, AIDS, renal carcinoma, cervical
 CC carcinoma, lymphoma, and condyloma acuminatum. The peptides may also be
 CC used to make monoclonal antibodies useful as potential diagnostic or
 CC therapeutic agents. The peptides may also be useful as diagnostic
 CC reagents, for example, to determine the susceptibility of an individual
 CC to a treatment regimen. Also, the peptides may be used to predict which
 CC individuals will be at substantial risk of developing chronic infection.
 CC The selection of appropriate T and B cell epitopes should allow the
 CC development of epitope based vaccines particularly towards conserved
 CC epitopes of pathogens which are characterized by high sequence
 CC variability such as HIV, HCV and Malaria.

XX Sequence 15 AA;

Query Match 100.0%; Score 43; DB 21; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.009;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIFCSLAFL 9

Db 3 kifgslafll 11

RESULT 9

R08222

ID R08222 standard; protein; 624 AA.

XX R08222;
 AC 06-MAR-1991 (first entry)
 DT Extracellular portion of the human epidermal growth factor receptor 2.
 DE Human epidermal growth factor receptor 2; HER2; vaccine; cancer.
 KW Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT Region 22..32
 FT /label= epitope
 FT /note= "potential T-cell epitope"
 FT Region 74..84
 FT /label= epitope
 FT /note= "potential T-cell epitope"
 FT Region 113..130
 FT /label= epitope
 FT /note= "potential T-cell epitope"
 FT Region 187..197
 FT /label= epitope
 FT /note= "potential T-cell epitope"
 FT Region 305..315
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 FT Region 327..353
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 FT Region 375..385
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 FT Region 398..408
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 FT Region 433..443
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 FT /note= "potential T-cell epitope"
 FT Region 519..529
 FT /label= epitope
 FT /note= "potential T-cell epitope"
 FT WO9014357-A.
 PN 29-NOV-1990.
 PD 18-MAY-1990; 90WO-US02697.
 XX 19-MAY-1989; 89US-0354319.
 XX (GETH) GENENTECH INC.
 XX Hudziak RM, Shepard HM, Ullrich A;
 XX WPI; 1990-375946/50.
 XX N-PSDB; Q06828.
 XX HER2 extracellular domain used as vaccine - comprises sequence of
 PT at least 9 amino acid(s) prep. using expression vector of DNA
 PT isolated from human epidermal growth factor receptor
 XX Disclosure; Fig 13; 49pp; English.
 XX This claimed sequence is free of transmembrane or intracellular
 CC portions of the HER2 mol. The protein is antigenic in animals.
 CC Fragment comprising at least 9 amino acids open several
 CC possibilities for further research and a broad range
 CC of potential therapeutic applications, e.g. for the treatment of
 CC mammary gland adenocarcinoma and other cancers.
 XX Sequence 624 AA;
 SQ

Query Match 100.0%; Score 43; DB 11; Length 624;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIFGSLAFL 9
|||||
DB 348 kifgslaf1 356

RESULT 10
W19764
ID W19764 standard; Protein: 782 AA.
XX
AC W19764;
XX
XX 17-SEP-1997 (first entry)
XX
DE Her2-GM-CSF immunostimulant fusion protein.

XX
KW Her2-GM-CSF; granulocyte macrophage colony stimulating factor;
KW growth factor receptor; oncogene; immunostimulant; cancer;
KW therapy.
XX
OS Homo sapiens.
XX

XX Key Location/Qualifiers
FH Protein 1..653
FT Peptide /label= Her2
FT Peptide 654..655
FT Protein /label= Linker
FT Protein 656..782
FT /label= GM-CSF
XX
PN WO9724438-A1.
XX
PD 10-JUL-1997.
XX
PF 23-DEC-1996; 96WO-US20241.
XX
PR 28-DEC-1995; 95US-0579823.
XX
XX (ACTT-) ACTIVATED CELL THERAPY INC.
PA
PI Laus R, Ruegg CL, Wu H;
XX
DR WPI: 1997-363674/33.
DR N-PSDB; T72725.
XX

PT Potent APC that activates T-cells to give multivalent cellular
PT immune response - can also induce a cytotoxic T-cell response in a
PT vertebrate subject
XX
PS Disclosure; Fig 8; 45pp; English.
XX

CC A fusion protein (W19764) comprises Her2 (a growth factor receptor
CC that is overexpressed in breast, ovarian and other cancer cells)
CC and granulocyte-macrophage colony stimulating factor (GM-CSF). It
CC is the expression product of a nucleic acid molecule (T72725). It
CC is prepared by PCR amplification of Her2 cDNA from a breast cancer cell
CC line and fusion to GM-CSF cDNA. Fusion expression vectors can be
CC used to transfect mammalian and insect cells. The Her2-GM-CSF
CC fusion protein is used to generate anti-Her2 immunity. Tumour
CC cells are eliminated by cytotoxic T lymphocytes activated in vivo
CC or in vitro by exposure to antigen-presenting cells exposed to the
CC fusion protein.
XX
SQ Sequence 782 AA;

Query Match 100.0%; Score 43; DB 18; Length 782;
Best Local Similarity 100.0%; Pred. No. 0.51; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIFGSLAFL 9
|||||
DB 369 kifgslaf1 377
RESULT 11
Y44993
ID Y44993 standard; Protein: 951 AA.
XX
AC Y44993;
XX
XX 23-MAY-2000 (first entry)
XX
DE DC8scFv-erbB2EC fusion protein containing tetramerisation domain.

XX
KW DC8 scFv; single-chain variable fragment; erbB2EC; extracellular domain;
KW human; fusion construct; tetramerisation domain; constant domain;
KW heteromultimer; multifunctional compound;
KW immunoglobulin; cytostatic; immunostimulatory; antileukaemia; diagnosis;
KW antiproliferative; prevention; treatment; malignant; haematopoietic cell;
KW lymphoma; leukaemia; solid tumour; carcinoma; melanoma; sarcoma.
XX

OS Chimeric - Unidentified.
OS Chimeric - Homo sapiens.
XX

XX Key Location/Qualifiers
FH Peptide 1..19
FT Region /label= Leader_sequence
FT Region 20..127
FT Region /label= DC8scFv_light_chain_variable_region
FT Region 128..142
FT Region /label= Glycine-Serine-linker
FT Region 143..254
FT Region /label= DC8scFv_heavy_chain_variable_region
FT Region 256..266
FT /note= "5' end of human IgG3 upper hinge region
FT with additional residues"
FT Domain 267..305
FT Peptide /label= Human_p53_tetramerisation_domain
FT Peptide 306..312
FT Domain /label= Short_peptide_linker
FT Domain 313..945
FT Region /label= erbB2EC_domain
FT Region 946..951
FT /label= His_tag
XX
PN WO200006605-A2.
XX
PD 10-FEB-2000.
XX
PF 28-JUL-1999; 99WO-EP05416.
XX
PR 28-JUL-1998; 98EP-0114082.
XX
XX (MICR-) MICROMET GES BIOMEDIZINISCHE FORSCHUNG.
XX
XX Kufer P, Dreier T, Baeuerle PA, Borschert K, Zettl F;
XX WPI: 2000-195265/17.
DR N-PSDB; Z50586.
XX
PT New multifunctional compounds useful for preventing and/or treating
PT malignant cell growth and for detection and diagnosis -
XX
PS Example 9; Fig 49; 166pp; English.
XX

CC The patent discloses heteromultimers which are multifunctional compounds
CC producible in a mammalian host cell as a secretable and fully functional
CC heterodimer of two polypeptide chains, where one of the polypeptide
CC chains comprises a CH1-domain (constant domain of an immunoglobulin
CC heavy chain) and the other chain comprises a C1-domain (constant domain of
CC an immunoglobulin light chain). The polypeptide chains further comprise,

CC fused to the constant domains at least two (poly)peptides having
 CC different receptor or ligand functions, where further at least two of the
 CC different (poly)peptides lack an intrinsic affinity for one another and
 CC are linked via the constant domains. The heteroantibodies have
 CC cytostatic, immunostimulatory, antileukaemia and antiproliferative
 CC activities. These compounds can be used for diagnosing, preventing and
 CC treating malignant cell growth related to malignancies of haematopoietic
 CC cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas,
 CC melanomas and sarcomas.
 CC The present sequence is a fusion protein comprising DC8
 CC single-chain Fv (scFv) fragment at the N-terminus, extracellular
 CC domain of human erbB2 at the C-terminus and a tetramerisation
 CC domain between them. This construct was prepared to find out whether
 CC an oligomerisation domain characterised in bacterial expression system
 CC is applicable for expression of fully functional and secretable
 CC recombinant protein in mammalian host cells. This tetrameric construct
 CC was not expressed as secretable and fully functional protein
 CC in mammalian cells. Hence general applicability of the tetramerisation
 CC domain for oligomerisation strategies in mammalian cells was ruled out.

XX
 SQ Sequence 951 AA;

Query Match 100.0%; Score 43; DB 21; Length 951;
 Best Local Similarity 100.0%; Pred. NO. 0.62; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0;

Qy 1 KIFGSLAPL 9
 |||||
 Db 660 kifgslaf1 668

RESULT 12

W01111
 ID W01111 standard; Protein; 1255 AA.

XX W01111;

DT 01-JAN-1997 (first entry)

DE HER-2/neu protein.

XX HER-2/neu; c-erbB1; p185; oncogene; tyrosine protein kinase;
 KW breast cancer; ovary cancer; colon cancer; lung cancer;
 KW prostate cancer; immunisation; tumour; vaccine; vector.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT Domain 676..1255

FT /label= Intracellular_domain
 FT /note= "claimed domain, useful for immunisation"

XX W09630514-A1.

XX 03-OCT-1996.

XX 28-MAR-1996; 96WO-US01689.

XX 31-MAR-1995; 95US-0414417.

XX (UNIW) UNIV WASHINGTON.

XX Cheever MA, Disis ML;

XX WPI; 1996-455361/45.

XX N-PSDB; T40739.

XX DNA encoding HER-2-neu poly:peptide(s) - used for prevention or
 PT treatment of malignancies with which the HER-2/neu oncogene is
 PT associated

XX Claim 2; Page 56-61; 71pp; English.

XX Human HER-2/neu protein (W01111), also called p185 or c-erbB2, is
 CC the product of the HER-2/neu oncogene (see also T40739). The
 CC protein is over-expressed in various cancers, including breast,
 CC ovarian, colon, lung and prostate. The intracellular domain of the
 CC protein can be used to immunise an animal against a malignancy with
 CC which the oncogene is associated. The polypeptide can be produced
 CC in transfected host cells for use in immunisation. Alternatively,
 CC animal cells are transfected in vivo or ex vivo with a viral vector
 CC that directs expression of the polypeptide.

XX Sequence 1255 AA;

Query Match 100.0%; Score 43; DB 17; Length 1255;
 Best Local Similarity 100.0%; Pred. NO. 0.83; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0;

Qy 1 KIFGSLAPL 9
 |||||
 Db 369 kifgslaf1 377

RESULT 13

W92406

ID W92406 standard; Protein; 1255 AA.

XX W92406;

DT 21-APR-1999 (first entry)

XX Human HER-2/neu oncogene protein.

XX HER-2/neu; oncogene; immune response; T cell; B cell; immunisation;
 KW malignancy; treatment; tumour.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT Region 676..1255

FT /note= "region which elicits immune response"

XX US5869445-A.

XX 09-FEB-1999.

XX 01-APR-1996; 96US-0625101.

XX 01-APR-1996; 96US-0625101.

XX 17-MAR-1993; 93US-0033644.

XX 12-AUG-1993; 93US-0106112.

XX 31-MAR-1995; 95US-0414417.

XX (UNIW) UNIV WASHINGTON.

XX Cheever MA, Disis ML;

XX WPI; 1999-152835/13.

XX N-PSDB; X01912.

XX Use of HER-2/neu polypeptides - for eliciting an immune response to
 PT an HER-2/neu associated malignancy, particularly for treating or
 PT preventing tumours

XX Claim 3; Column 31-38; 26pp; English.

XX This sequence represents the human HER-2/neu oncogene protein. A fragment
 CC of this protein is used in a method for eliciting or enhancing an immune
 CC response to HER-2/neu protein. The polypeptide can stimulate T cells and
 CC B cells to produce an immune response to the HER-2/neu protein. The
 CC method can be used for immunisation against a malignancy in which the
 CC HER-2/neu oncogene is associated and in the treatment of an existing
 CC tumour, or to prevent tumour occurrence or reoccurrence.

```

XX SQ Sequence 1255 AA;
Query Match 100.0%; Score 43; DB 20; Length 1255;
Best Local Similarity 100.0%; Pred. No. 0.83;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIFGSLAFL 9
Db 369 kifgslaf1 377
|||||

RESULT 14
Y84780
ID Y84780 standard; Protein; 1255 AA.
XX
AC Y84780;
XX
DT 08-AUG-2000 (first entry)
XX
DE Amino acid sequence of the SPLICE erbb-2 receptor protein.
XX
KW SPLICE erbb-2 receptor protein; cell transformation disorder; cancer;
KW tumor cell proliferation; tissue degeneration; arthropathy;
KW bone resorption; inflammatory disease; degenerative disorder;
KW wound healing.
XX
OS Homo sapiens.
XX
PN W0200020579-A1.
XX
PD 13-APR-2000.
XX
PE 01-OCT-1999; 99WO-CA00912.
XX
PR 02-OCT-1998; 98US-0165192.
XX
PA (UYMC-) UNIV MCMASTER.
XX
PI Muller WJ, Siegel PM;
XX
XX WPT; 2000-303768/26.
DR N-PSDB; A14812.
XX
XX Nucleic acid encoding an erbb 2 receptor protein designated SPLICE
PT erbb-2, inhibitors of the protein are useful for treatment of cancer -
PT
PS Claim 3; Fig 2; 60pp; English.
XX
CC The present sequence represents a SPLICE erbb-2 receptor protein. The
CC protein has an in-frame deletion of 16 amino acids, 2 of which are
CC conserved cysteine residues, compared to the unspliced protein. The
CC erbb-2 polynucleotide is used to construct probes for detecting
CC disorders of cell transformation such as cancer. Antibodies to the
CC protein may be used to detect SPLICE erbb-2 in a sample. Agents
CC (e.g. antisense oligonucleotides) which inhibit the expression of
CC SPLICE erbb-2 are useful for reducing tumor cell proliferation and
CC treating cancer. Substances which stimulate SPLICE erbb-2 are useful
CC for treating conditions involving damaged cells including conditions
CC in which degeneration of tissue occurs, such as arthropathy, bone
CC resorption, inflammatory diseases, degenerative disorders of the
CC central nervous system and wound healing.
XX
SQ Sequence 1255 AA;
Query Match 100.0%; Score 43; DB 21; Length 1255;
Best Local Similarity 100.0%; Pred. No. 0.83;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIFGSLAFL 9
Db 369 kifgslaf1 377
|||||

RESULT 15
Y92620
ID Y92620 standard; Protein; 1255 AA.
XX
AC Y92620;
XX
DT 10-AUG-2000 (first entry)
XX
DE Human heregulin 2 (Her2).
XX
KW Heregulin 2; Her2; vaccination; cytotoxic T-lymphocyte immunity;
KW self-protein; cancer; breast cancer; prostate cancer;
KW cell-associated peptide antigen; foreign epitope.
XX
OS Homo sapiens.
XX
FH Key
FH Domain
FT 1..173
FT /label= N-terminal
FT /note= "mature polypeptide"
FT
FT 5..25
FT /label= insertion_region
FT /note= "suitable for foreign epitope insertion"
FT
FT 59..73
FT /label= insertion_region
FT /note= "suitable for foreign epitope insertion"
FT
FT 103..117
FT /label= insertion_region
FT /note= "suitable for foreign epitope insertion"
FT
FT 149..163
FT /label= insertion_region
FT /note= "suitable for foreign epitope insertion"
FT
FT 174..323
FT /label= Cysteine_rich_domain
FT
FT 210..224
FT /label= insertion_region
FT /note= "suitable for foreign epitope insertion"
FT
FT 250..264
FT /label= insertion_region
FT /note= "suitable for foreign epitope insertion"
FT
FT 324..483
FT /label= Ligand_binding_domain
FT
FT 325..339
FT /label= insertion_region
FT /note= "suitable for foreign epitope insertion"
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FT 369..383
FT /label= insertion_region
FT /note= "suitable for foreign epitope insertion"
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FT 465..479
FT /label= insertion_region
FT /note= "suitable for foreign epitope insertion"
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FT 484..623
FT /label= Cysteine_rich_domain
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FT 579..593
FT /label= insertion_region
FT /note= "suitable for foreign epitope insertion"
FT
FT 624..654
FT /label= Transmembrane_domain
FT
FT 632..652
FT /label= insertion_region
FT /note= "suitable for foreign epitope insertion"
FT
FT 653..667
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FT /note= "suitable for foreign epitope insertion"
FT
FT 655..1010
FT /label= Tyrosine_Kinase_domain
FT
FT 661..675
FT /label= insertion_region
FT /note= "suitable for foreign epitope insertion"
FT
FT 695..709
FT /label= insertion_region
FT /note= "suitable for foreign epitope insertion"
FT

```

FT /label= insertion_region
FT /note= "suitable for foreign epitope insertion"
FT 710..730
FT /label= insertion_region
FT /note= "suitable for foreign epitope insertion"
FT 1011..1235
FT /label= C-terminal_domain
XX
PN WO200020027-A2.
XX
XX 13-APR-2000.
XX
XX 05-OCT-1999; 99WO-DK00525.
XX
XX 05-OCT-1998; 98DK-0001261.
PR 20-OCT-1998; 98US-0105011.
XX
XX (MEBI-) M & E BIOTECH AS.
XX
XX Steinaa L, Mouritsen S, Nielsen KG, Haaning J, Leach D, Dalum I;
PI Gautam A, Birk P, Karlsson G;
XX
XX WPI; 2000-349917/30.
DR N-PSDB; A09455.
XX
XX
FT Inducing immune responses to weakly immunogenic, tumor associated
PT peptide antigens for the treatment of breast and prostate cancer
XX
XX Claim 62; Page 193-198; 220pp; English.
XX
CC This is the human heregulin 2 (Her2) sequence. Immunogenic analogues of
CC Her2 can be used in the claimed method as an autovaccine to induce a CTL
CC response. Subdominant CTL epitopes, antibody binding regions and
CC cysteine residues involved in disulfide bonds are preserved in the
CC immunogenized forms. Regions suitable for the insertion of foreign T
CC helper epitopes were identified (see features table). The method
CC is used for inducing immune responses against weakly immunogenic
CC cell-associated peptide antigens (PA) such as those associated with
CC cancers (self-proteins), e.g. human prostate specific membrane antigen
CC (PSM), heregulin 2 (Her2) and/or fibroblast growth factor 8b (FGF8b).
CC The method comprises effecting simultaneous presentation by antigen
CC producing cells (APCs) of the animals immune system of: (1) at least 1
CC CTL (cytotoxic T-lymphocyte) group derived from the PA and/or at least 1
CC B-cell group derived from the cell-associated PA; and (2) at least 1
CC first T helper cell group which is foreign to the animal. Analogues of
CC human PSM, human Her2 and human/murine FGF8b comprising a substantial
CC part of all known and predicted CTL and B-cell epitopes of the respective
CC PA and including at least one foreign T helper epitope are also claimed.
CC The method is used to treat prostate, prostate/breast or breast cancer
CC when the PA is human PSM, FGF8b and Her2, respectively.
XX
SQ Sequence 1255 AA;

Query Match 100.0%; Score 43; DB 21; Length 1255;
Best Local Similarity 100.0%; Pred. No. 0.83;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KIFGSLAFL 9
| | | | |
Db 369 kifgslaf1 377

Search completed: November 14, 2000, 11:55:20
Job time: 38 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 14, 2000, 11:54:42 ; Search time 12.27 Seconds
(without alignments)
12.294 Million cell updates/sec

Title: US-09-277-074-10

Perfect score: 43

Sequence: 1 KIFGSLAFL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 164575 seqs, 16761186 residues

Total number of hits satisfying chosen parameters: 164575

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued_Patents_AA.*
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep.*
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3: /cgn2_6/ptodata/2/1aa/6_COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	100.0	9	1	US-08-467-083-27
2	43	100.0	9	1	US-08-787-547-70
3	43	100.0	9	1	US-08-414-417B-27
4	43	100.0	9	2	US-08-486-348A-27
5	43	100.0	9	2	US-08-468-545B-27
6	43	100.0	9	2	US-08-902-516-18
7	43	100.0	9	3	US-08-466-680B-27
8	43	100.0	9	4	PCT-US95-16415-10
9	43	100.0	16	1	US-08-467-083-62
10	43	100.0	16	1	US-08-414-417B-62
11	43	100.0	16	2	US-08-486-348A-62
12	43	100.0	16	2	US-08-468-545B-62
13	43	100.0	16	3	US-08-466-680B-62
14	43	100.0	624	3	US-08-422-108-1
15	43	100.0	782	2	US-09-146-283-4
16	43	100.0	782	3	US-08-579-823A-4
17	43	100.0	1255	1	US-08-467-083-68
18	43	100.0	1255	1	US-08-414-417B-68
19	43	100.0	1255	2	US-08-484-438-8
20	43	100.0	1255	2	US-08-486-348A-68
21	43	100.0	1255	2	US-08-625-101-2
22	43	100.0	1255	2	US-08-468-545B-68
23	43	100.0	1255	2	US-08-356-786-2
24	43	100.0	1255	3	US-08-466-680B-68
25	30	69.8	269	1	US-08-118-270-64
26	30	69.8	269	4	PCT-US93-08528-64
27	30	69.8	790	3	US-08-537-361E-8
28	30	69.8	791	3	US-08-537-361E-4

29 30 59.8 792 1 US-08-326-670A-2 Sequence 2, Appli
30 30 59.8 792 3 US-08-537-361E-2 Sequence 2, Appli
31 30 59.8 792 3 US-08-537-361E-6 Sequence 6, Appli
32 29 67.4 15 1 US-08-467-083-36 Sequence 36, Appli
33 29 67.4 15 1 US-08-414-417B-36 Sequence 36, Appli
34 29 67.4 15 2 US-08-486-348A-36 Sequence 36, Appli
35 29 67.4 15 2 US-08-468-545B-36 Sequence 36, Appli
36 29 67.4 15 3 US-08-466-680B-36 Sequence 36, Appli
37 29 67.4 24 1 US-08-103-445-21 Sequence 21, Appli
38 29 67.4 24 1 US-08-461-690B-21 Patent No. 5447867
39 29 67.4 457 5 5447867-1 Sequence 12, Appli
40 29 67.4 711 3 US-08-772-270A-12 Sequence 5, Appli
41 28 65.1 182 2 US-08-558-823-5 Sequence 1, Appli
42 28 65.1 185 1 US-08-233-389C-1 Sequence 1, Appli
43 28 65.1 185 2 US-08-801-863-1 Sequence 1, Appli
44 28 65.1 185 2 US-08-486-596A-1 Sequence 1, Appli
45 28 65.1 185 2 US-09-004-713-1 Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-467-083-27
; Sequence 27, Application US/08467083
; Patent No. 5726023

GENERAL INFORMATION:

APPLICANT: Cheever, Martin A.

APPLICANT: Disis, Mary L.

TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN

TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
HER-2/NEU ONCOGENE IS ASSOCIATED

NUMBER OF SEQUENCES: 68

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed and Berry

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: US

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/467,083

FILING DATE: 06-JUN-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/414,417

FILING DATE: 06-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Sharkey, Richard G.

REGISTRATION NUMBER: 32,629

REFERENCE/DOCKET NUMBER: 920010.448C2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

TELEX: 3723836 SEEDANBERRY

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

US-08-467-083-27

Query Match 100.0%; Score 43; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIFGSLAFL 9
| | | | | | | |
Db 1 KIFGSLAFL 9

RESULT 2

US-08-787-547-70
; Sequence 70, Application US/08787547
; Patent No. 5783567
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Curley, Joanne M.
; APPLICANT: Langer, Robert S.
; TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY
; TITLE OF INVENTION: OF NUCLEIC ACID
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/787,547
; FILING DATE: 22-JAN-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/003001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-787-547-70

Query Match 100.0%; Score 43; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIFGSLAFL 9
| | | | | | | |
Db 1 KIFGSLAFL 9

RESULT 3

US-08-414-417B-27
; Sequence 27, Application US/0841417B
; Patent No. 5801005
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,348A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900

; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,417B
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-414-417B-27

Query Match 100.0%; Score 43; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIFGSLAFL 9
| | | | | | | |
Db 1 KIFGSLAFL 9

RESULT 4

US-08-486-348A-27
; Sequence 27, Application US/08486348A
; Patent No. 5846538
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,348A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900

```
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-466-348A-27

Query Match 100.0%; Score 43; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIFGSLAFL 9
Db 1 KIFGSLAFL 9

RESULT 5
US-08-468-545B-27
; Sequence 27, Application US/08468545B
; Patent No. 5876712
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,545B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C5
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-468-545B-27

Query Match 100.0%; Score 43; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIFGSLAFL 9
Db 1 KIFGSLAFL 9

RESULT 6
US-08-902-516-18
; Sequence 18, Application US/08902516
; Patent No. 5891432
; GENERAL INFORMATION:
; APPLICANT: Soo Hoo, William
; TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS
; TITLE OF INVENTION: COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE
; TITLE OF INVENTION: RESPONSE USING SAME
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL & FLORES, LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/902,516
; FILING DATE: 29-JUL-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IM 2442
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)535-9001
; TELEFAX: (619)535-8949
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-902-516-18

Query Match 100.0%; Score 43; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIFGSLAFL 9
Db 1 KIFGSLAFL 9

RESULT 7
US-08-466-680B-27
; Sequence 27, Application US/08466680B
; Patent No. 6075122
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
```

```

: APPLICATION NUMBER: US/08/466,680B
: FILING DATE: 06-JUN-1995
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: Sharkey, Richard G.
: REGISTRATION NUMBER: 32,629
: REFERENCE/DOCKET NUMBER: 920010.448C4
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206) 622-4900
: TELEFAX: (206) 682-6031
: INFORMATION FOR SEQ ID NO: 21:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 9 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear
US-08-466-680B-27

```

Query Match 100.0%; Score 43; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. NO. 1.2e+05;
Matches 9; Conservative 0; Mismatches 0; Indels

Qy 1 KIFGSLAFL 9
| | | | | | | |
Db 1 KIFGSLAFL 9

RESULT 8
PCT-US95-16415-10
; Sequence 10, Application PC/TUS9516415
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: IN VIVO ACTIVATION OF TUMOR-SPECIFIC
; TITLE OF INVENTION: CYTOTOXIC T CELLS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute
; STREET: 10666 North Torrey Pines Road, TPC-8
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037

```
Query Match      100.0%; Score 43; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
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Matches      9;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

Qy      1  KIFGSLAFL 9
|||||||
Db      1  KIFGSLAFL 9

RESULT      9
US-08-467-083-62
; Sequence 62, Application US/08467083
; Patent NO. 5726023

```

Query Match 100.0%; Score 43; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 9; Conservative 0; Mismatches 0; Indels

Qy 1 KIFGSLAFL 9
| | | | | | | |
Db 1 KIFGSLAFL 9

RESULT 10
US-08-414-417B-62
; Sequence 62, Application US/08414417B
; Patent No. 5801005
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY
; TITLE OF INVENTION: FOR DIAGNOSIS
; TITLE OF INVENTION: HER-2/neu ONCO

NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/414.417B
FILING DATE: 31-MAR-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C2
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-414-417B-62

Query Match 100.0%; Score 43; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIFGSLAFL 9
|||||
Db 1 KIFGSLAFL 9

RESULT 11
US-08-486-348A-62
Sequence 62, Application US/08486348A
Patent No. 5846538
GENERAL INFORMATION:
APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486.348A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C5

TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-486-348A-62

Query Match 100.0%; Score 43; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIFGSLAFL 9
|||||
Db 1 KIFGSLAFL 9

RESULT 12
US-08-468-545B-62
Sequence 62, Application US/08468545B
Patent No. 5876712
GENERAL INFORMATION:
APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468.545B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C5
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-468-545B-62

Query Match 100.0%; Score 43; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIFGSLAFL 9
|||||
Db 1 KIFGSLAFL 9

RESULT 13
US-08-466-680B-62
; Sequence 62, Application US/08466680B
; Patent No. 6075122
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,680B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-466-680B-62

Query Match 100.0%; Score 43; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIFGSLAFL 9
| | | | | | | |
Db 1 KIFGSLAFL 9

RESULT 14
US-08-422-108-1
; Sequence 1, Application US/08422108
; Patent No. 6015567
; GENERAL INFORMATION:
; APPLICANT: Hudziak, Robert M.
; APPLICANT: Shepard, H. Michael
; APPLICANT: Ullrich, Axel
; TITLE OF INVENTION: HER2 EXTRACELLULAR DOMAIN
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,108
; FILING DATE: 14-Apr-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/355460
; FILING DATE: 13-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/048346
; FILING DATE: 15-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/354319
; FILING DATE: 19-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 554C2D2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 624 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-422-108-1

Query Match 100.0%; Score 43; DB 3; Length 624;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIFGSLAFL 9
| | | | | | | |
Db 348 KIFGSLAFL 356

RESULT 15
US-09-146-283-4
; Sequence 4, Application US/09146283
; Patent No. 5976546
; GENERAL INFORMATION:
; APPLICANT: Laus, Reiner
; APPLICANT: Ruegg, Curtis L.
; APPLICANT: Wu, Hongyu
; TITLE OF INVENTION: Immunostimulatory Compositions
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave. Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/146,283
; FILING DATE: 03-SEPT-1998
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Judge, Linda R.
; REGISTRATION NUMBER: 42,702
; REFERENCE/DOCKET NUMBER: 7636-0010.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 782 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: homo sapiens
INDIVIDUAL ISOLATE: GM-CSF-Her-2 fusion protein; Fig. 8
US-09-146-283-4

Query Match 100.0%; Score 43; DB 2; Length 782;
Best Local Similarity 100.0%; Pred. NO. 0.42;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIFGSLAFL 9
|||||||
Db 369 KIFGSLAFL 377

Search completed: November 14, 2000, 11:55:00
Job time: 18 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 14, 2000, 11:54:42 ; Search time 13.48 Seconds
(without alignments)
42.370 Million cell updates/sec

Title: US-09-277-074-10
Perfect score: 43
Sequence: 1 KIFGSLAFL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 182106 seqs, 53460219 residues

Total number of hits satisfying chosen parameters: 182106

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_65:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	100.0	1254	2 148161	p-185 precursor -
2	43	100.0	1255	1 A24571	protein-tyrosine k
3	43	100.0	1260	1 TVRPNU	protein-tyrosine k
4	36	83.7	336	2 T28747	hypothetical prote
5	36	83.7	502	2 G71055	hypothetical prote
6	34	79.1	298	2 S53849	ribosomal protein
7	34	79.1	370	2 T48578	hypothetical prote
8	34	79.1	540	2 S56215	probable membrane
9	33	76.7	120	2 T16442	hypothetical prote
10	33	76.7	449	2 F81954	cytochrome B (EC 1
11	33	76.7	449	2 E81011	ubiquinol--cytochr
12	32	74.4	157	2 S58038	probable olfactory
13	32	74.4	231	2 T20347	hypothetical prote
14	32	74.4	298	2 S60649	NADH dehydrogenase
15	32	74.4	323	2 S05035	protein kinase (EC
16	32	74.4	434	2 T27040	hypothetical prote
17	32	74.4	671	1 OKBOG	protein kinase (EC
18	32	74.4	686	1 S05702	protein kinase (EC
19	32	74.4	758	2 S62432	major facilitator
20	32	74.4	1029	2 S56229	probable membrane
21	31	72.1	138	2 A6S187	hypothetical 15.4
22	31	72.1	149	2 T28298	ORF MSV137 hypothe
23	31	72.1	232	2 H69173	conserved hypothet
24	31	72.1	240	2 E70771	hypothetical prote
25	31	72.1	251	2 S72791	hypothetical prote
26	31	72.1	264	2 E72119	conserved hypothet
27	31	72.1	326	2 E72282	oligopeptide ABC t
28	31	72.1	335	2 T20920	hypothetical prote
29	31	72.1	343	2 T33989	hypothetical prote

30	31	72.1	350	2 T28975	hypothetical prote
31	31	72.1	475	2 F71419	probable indole-3-
32	31	72.1	505	2 T26764	hypothetical prote
33	31	72.1	573	2 S60912	probable transport
34	31	72.1	686	2 A45483	chloride channel,
35	31	72.1	687	2 A57713	chloride channel C
36	31	72.1	687	2 D57713	chloride channel C
37	31	72.1	687	2 C57713	chloride channel C
38	31	72.1	956	2 S64449	centromere-binding
39	31	72.1	965	2 T32574	hypothetical prote
40	31	72.1	1483	2 S42839	Ti6G12.5 protein -
41	31	72.1	3848	2 T17414	tipC protein - sll
42	31	72.1	4199	2 S76412	hypothetical prote
43	30.5	70.9	3351	2 T13812	lipophorin - fruit
44	30	69.8	51	2 T07326	hypothetical prote
45	30	69.8	77	2 A72256	hypothetical prote

ALIGNMENTS

RESULT 1
I48161
p-185 precursor - golden hamster
C:Species: Mesocricetus auratus (golden hamster)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 18-Jun-1999
C:Accession: I48161
R:Nakamura, T.; Ushijima, T.; Ishizaka, Y.; Nagao, M.; Arai, M.; Yamazaki, Y.; Ishika
Gene 140, 251-255, 1994
A:Title: Cloning and activation of the Syrian hamster neu proto-oncogene.
A:Reference number: I48161; MUID:94193007
A:Accession: I48161
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1254 <RES>
A:Cross-references: GB:D16295; NID:g493236; PIDN:BAA03801.1; PID:g747595
C:Genetics:
A:Gene: neu
C:Superfamily: epidermal growth factor receptor; protein kinase homology
C:Keywords: Atp
F:718-983/Domains: protein kinase homology <KIN>
F:726-734/Region: protein kinase Atp-binding motif

Query Match 100.0%; Score 43; DB 2; Length 1254;
Best Local Similarity 100.0%; Pred. No. 0.72; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 1 KIFGSLAFL 9
| | | | | | | | | |
Db 369 KIFGSLAFL 377

RESULT 2
A24571
protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - human
N:Alternate names: c-erb-B-2 protein precursor; kinase-related transforming protein e
C:Species: Homo sapiens (man)
C:Date: 25-Oct-1987 #sequence_revision 06-Dec-1996 #text_change 11-Jun-1999
C:Accession: A24571; A25491; A44188; B44188; I59509; I57622
R:Yamamoto, T.; Ikawa, S.; Akiyama, T.; Semba, K.; Nomura, N.; Miyajima, N.; Salto, T
Nature 319, 230-234, 1986
A:Title: Similarity of protein encoded by the human c-erb-B-2 gene to epidermal growth
A:Reference number: A24571; MUID:86118663
A:Accession: A24571
A:Molecule type: mRNA
A:Residues: 1-1255 <YAM>
A:Cross-references: GB:X03363; NID:g31197; PIDN:CAA27060.1; PID:g31198
R:Semba, K.; Kamata, N.; Toyoshima, K.; Yamamoto, T.
Proc. Natl. Acad. Sci. U.S.A. 82, 6497-6501, 1985
A:Title: A v-erbB-related protooncogene, c-erbB-2, is distinct from the c-erbB-1/epid
A:Reference number: A25491; MUID:86016729
A:Accession: A25491

A:Molecule type: DNA
 A:Residues: 737-1031 <SEM>
 A:Cross-references: GB:M11767; NID:gl82163; PIDN:AAA35808.1; PID:g553282
 R:Cousens, L.; Yang-Feng, T.L.; Liao, Y.C.; Chen, E.; Gray, A.; McGrath, J.; Seeburg, P.
 Science 230, 1132-1139, 1985
 A>Title: Tyrosine kinase receptor with extensive homology to EGF receptor shares chromo-
 A:Reference number: A44188; MUID:86070181
 A:Accession: A44188
 A:Molecule type: DNA
 A:Residues: 740-910 <COU1>
 A:Cross-references: GB:M12036; NID:gl83988; PIDN:AAA35978.1; PID:gl83989
 A:Accession: B44188
 A:Molecule type: mRNA
 A:Residues: 1-517, 'HALL', 522, 'S', 524-654, 'V', 656-1169, 'A', 1171-1255 <COU2>
 A:Cross-references: GB:M11730; NID:gl83986
 R:King, C.R.; Kraus, M.H.; Aaronson, S.A.
 Science 229, 974-976, 1985
 A>Title: Amplification of a novel v-erbB-related gene in a human mammary carcinoma.
 A:Reference number: I59509; MUID:85272597
 A:Accession: I59509
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 832-909 <REX>
 A:Cross-references: GB:L29395; NID:q459807; PIDN:AAA35809.1; PID:q459808
 R:Yai, M.; King, C.R.; Kraus, M.H.; Ullrich, A.; Schlessinger, J.; Givol, D.
 Mol. Cell. Biol. 7, 2597-2601, 1987
 A>Title: Human HER2 (neu) promoter: evidence for multiple mechanisms for transcriptional
 A:Reference number: I57622; MUID:87286898
 A:Accession: I57622
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-191 <PAL>
 A:Cross-references: GB:M16792; NID:gl83983; PIDN:AAA58637.1; PID:g553332
 C:Comment: Amplification and overexpression of this erbB-related gene occurs in about 30
 C:Genetics:
 A:Gene: GDB:ERBB2; NGL; NEU; HER-2
 A:Cross-references: GDB:L20613; OMIM:164870
 A:Map position: 17q21.1-17q21.1
 A:Introns: 25/1; 75/3; 147/1; 883/3
 A>Note: the list of introns is incomplete
 C:Function:
 A:Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
 C:Superfamily: epidermal growth factor receptor; protein kinase homology
 C:Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; phospho-
 inase
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:22-1255/Product: protein-tyrosine kinase erbB2 #status predicted <MAT>
 F:22-653/Domain: extracellular #status predicted <EXT>
 F:70-304/Domain: EGF receptor extracellular domain repeat <EEL>
 F:395-605/Domain: EGF receptor extracellular domain repeat <EE2>
 F:654-675/Domain: transmembrane #status predicted <TMW>
 F:676-1255/Domain: intracellular #status predicted <INT>
 F:718-983/Domain: protein kinase homology <KIN>
 F:726-734/Region: protein kinase ATP-binding motif
 F:68,124,187,259,530,571,629/Binding site: carboxylate (Asn) (covalent) #status predict
 F:686/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
 F:753/Active site: Lys #status predicted
 F:1139,1221,1222,1248/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation)

Query Match 100.0%; Score 43; DB 1; Length 1255;
 Best Local Similarity 100.0%; Pred. No. 0.72;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIFGSLAFL 9
 |||||

Db 369 KIFGSLAFL 377

RESULT 3

TVRTNU

protein-tyrosine kinase (EC 2.7.1.112) neu precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 11-Jun-1999
 C:Accession: A24562; A61204
 R:Bargmann, C.I.; Hung, M.C.; Weinberg, R.A.
 Nature 319, 226-230, 1986
 A>Title: The neu oncogene encodes an epidermal growth factor receptor-related protein
 A:Reference number: A24562; MUID:86118662
 A:Accession: A24562
 A:Molecule type: mRNA
 A:Residues: 1-1260 <BAR>
 A:Cross-references: EMBL:X03362; NID:g56745; PIDN:CAA27059.1; PID:g56746
 R:Masui, T.; Mann, A.M.; Macatee, T.L.; Garland, E.M.; Okamura, T.; Smith, R.A.; Cohen
 Carcinogenesis 12, 1975-1978, 1991
 A>Title: Direct DNA sequencing of the rat neu oncogene transmembrane domain reveals n
 2-thiazolyl]formamide or N-methyl-N-nitrosourea.
 A:Reference number: A61204; MUID:92035293
 A:Accession: A61204
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 637-663, 'V', 665-702 <MAS>
 A>Note: authors translated the codon GCA for residue 25 as Val
 C:Genetics:
 A:Gene: neu
 C:Superfamily: epidermal growth factor receptor; protein kinase homology
 C:Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; phos
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-1260/Product: protein-tyrosine kinase neu #status predicted <MAT>
 F:658-680/Domain: transmembrane #status predicted <TMW>
 F:723-988/Domain: protein kinase homology <KIN>
 F:731-739/Region: protein kinase ATP-binding motif
 F:71,191,263,535,576,634/Binding site: carboxylate (Asn) (covalent) #status predict
 F:691/Binding site: phosphate (Thr) (covalent) #status predicted
 F:758/Active site: Lys #status predicted
 F:882,1227,1253/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 100.0%; Score 43; DB 1; Length 1260;
 Best Local Similarity 100.0%; Pred. No. 0.72;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIFGSLAFL 9
 |||||

Db 373 KIFGSLAFL 381

RESULT 4

T28747

hypothetical protein F48G7.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999

C:Accession: T28747

R:Clarke, K.; Wohldmann, P.; Harrison, M.

submitted to the EMBL Data Library, January 1998

A:Description: The sequence of C. elegans cosmid F48G7.

A:Reference number: Z20517

A:Accession: T28747

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-356 <CLA>

A:Cross-references: EMBL:AF039044; PIDN:AC47951.1; GSPDB:GN00023; CESP:F48G7.1
 A:Experimental source: strain Bristol N2; clone F48G7

C:Genetics:

A:Gene: CESP:F48G7.1

A:Map position: 5

A:Introns: 64/3; 148/3; 220/1; 301/2

Query Match 83.7%; Score 36; DB 2; Length 356;
 Best Local Similarity 66.7%; Pred. No. 6.1;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIFGSLAFL 9
 |||||

Db 13 KIFGSLAFL 21

RESULT 5

hypothetical protein PH1141 - Pyrococcus horikoshii
 G71055
 C:Species: Pyrococcus horikoshii
 C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
 C:Accession: G71055
 R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
 M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
 DNA Res. 5, 55-76, 1998
 A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
 A:Reference number: A71000; MUID:98344137
 A:Accession: G71055
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-502 <KAW>
 A:Cross-references: GB:AP000005; NID:g3236132; PIDN:BAA30241.1; PID:g3257558
 A:Experimental source: strain OT3
 A:Note: this accession replaces an interim accession for a sequence replaced by GenBank
 C:Genetics:
 A:Gene: PH1141
 C:Superfamily: Pyrococcus horikoshii hypothetical protein PH1141

Query Match

Best Local Similarity 83.7%; Score 36; DB 2; Length 502;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IFGSLAFL 9

Db 123 IFGSLAFL 130

RESULT 6

ribosomal protein S3 - Acanthamoeba castellanii mitochondrion
 S53849
 C:Species: mitochondrion Acanthamoeba castellanii
 C:Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 07-Dec-1999
 C:Accession: S53849
 R:Burger, G.; Plante, I.; Loneragan, K.M.; Gray, M.W.
 J. Mol. Biol. 245, 522-537, 1995
 A:Title: The mitochondrial DNA of the amoeboid protozoan, Acanthamoeba castellanii: comp
 A:Reference number: S53825; MUID:95147275
 A:Accession: S53849
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-298 <BUR>

A:Cross-references: GB:U12386; NID:g562028; PID:g562053

A:Experimental source: strain Neff; AFCC 30010
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994

C:Genetics:

A:Genome: mitochondrion

A:Genetic code: SGC6

C:Keywords: mitochondrion

Query Match

Best Local Similarity 79.1%; Score 34; DB 2; Length 298;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KIFGSLAF 8

Db 250 KAFGSLAF 257

RESULT 7

hypothetical protein T31B5.130 - Arabidopsis thaliana
 T48578
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
 C:Accession: T48578
 R:Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft,

submitted to the Protein Sequence Database, April 2000

A:Reference number: Z24490

A:Accession: T48578

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-370 <BEV>

A:Cross-references: EMBL:AL163491

A:Experimental source: cultivar Columbia; BAC clone T31B5

C:Genetics:

A:Map position: 5

A:Introns: 119/3

A:Note: T31B5.130

Query Match

Best Local Similarity 79.1%; Score 34; DB 2; Length 370;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KIFGSLAF 8

Db 17 KIFGSLPF 24

RESULT 8

S56215
 probable membrane protein YFL040w - yeast (Saccharomyces cerevisiae)
 N:Alternate names: protein R004

C:Species: Saccharomyces cerevisiae

C:Date: 02-Sep-1995 #sequence_revision 19-Oct-1995 #text_change 20-Jun-2000

C:Accession: S56215; S60496

R:Murakami, Y.; Naitou, M.; Haglward, H.; Shibata, T.; Ozawa, M.; Sasanuma, S.I.; Sas

submitted to the EMBL Data Library, May 1995

A:Description: Analysis of the nucleotide sequence of chromosome VI from Saccharomyces

A:Reference number: S56186

A:Accession: S56215

A:Molecule type: DNA

A:Residues: 1-540 <MUR>

A:Cross-references: EMBL:D50617; NID:g836685; PID:g836715; MIPS:YFL040w

R:Naitou, M.; Ozawa, M.; Sasanuma, S.I.; Kobayashi, M.; Haglward, H.; Shibata, T.; Ha

Yeast 11, 1525-1532, 1995

A:Title: Sequencing of an 18.8 kb fragment from Saccharomyces cerevisiae chromosome V

A:Reference number: S60495; MUID:96353435

A:Accession: S60496

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-540 <NAI>

A:Cross-references: EMBL:D44598; NID:g871933; PID:g1100781

C:Genetics:

A:Map position: 6L

C:Superfamily: glucose transport protein

C:Keywords: transmembrane protein

F:25-41/Domain: transmembrane #status predicted <TM1>

F:69-85/Domain: transmembrane #status predicted <TM2>

F:107-123/Domain: transmembrane #status predicted <TM3>

F:161-177/Domain: transmembrane #status predicted <TM4>

F:184-200/Domain: transmembrane #status predicted <TM5>

F:291-307/Domain: transmembrane #status predicted <TM6>

F:318-334/Domain: transmembrane #status predicted <TM7>

F:341-357/Domain: transmembrane #status predicted <TM8>

F:391-407/Domain: transmembrane #status predicted <TM9>

F:429-445/Domain: transmembrane #status predicted <TM10>

F:457-473/Domain: transmembrane #status predicted <TM11>

Query Match

Best Local Similarity 79.1%; Score 34; DB 2; Length 540;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 IFGSLAFL 9

Db 459 IFGSLTFL 466

RESULT 11
E81011
ubiquinol--cytochrome c reductase, cytochrome b NMB2052 [imported] - Neisseria meningitidis
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 31-Mar-2000
C:Accession: E81011
R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Qi, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.; Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; V

Query Match 74.4%; Score 32; DB 2; Length 231;
Best Local Similarity 62.5%; Pred. NO. 27;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIFGSLAF 8
 ::|||::||
 DB 44 QVFGSI AF 51

RESULT 14

S60649

NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 - brine shrimp mitochondrion
 C:Species: mitochondrion Artemia franciscana (brine shrimp)

C>Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 07-Dec-1999

C:Accession: S60649

R:Perez, M.L.; Valverde, J.R.; Batuecas, B.; Amat, F.; Marco, R.; Garesse, R.

J. Mol. Evol. 38, 156-168, 1994

A:Title: Speciation in the Artemia genus: mitochondrial DNA analysis of bisexual and par-

A:Reference number: S60624; MUID:94223692

A:Accession: S60649

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-298 <PER>

A:Cross-references: EMBL:X69067; NID:9505262; PIDN:CAA48818.1; PID:9578449

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1994

C:Genetics:

A:Gene: ND-1

A:Genome: mitochondrion

A:Genetic code: SGC4

C:Superfamily: NADH dehydrogenase (ubiquinone) chain 1

C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match

74.4% Score 32; DB 2; Length 298;

Best Local Similarity 62.5%; Pred. No. 35;

Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 IFGSLAF 9

::|||::||

DB 241 VFGSMFL 248

RESULT 15

S05035

protein kinase (EC 2.7.1.37), cGMP-dependent, form I-beta - bovine (fragments)

C:Species: Bos primigenius taurus (cattle)

C>Date: 07-Sep-1990 #sequence_revision 24-Feb-1995 #text_change 04-Feb-2000

C:Accession: S05035; A32952; A60180

R:Wernet, W.; Flockerzi, V.; Hofmann, F.

FEBS Lett. 251, 191-196, 1989

A:Title: The cDNA of the two isoforms of bovine cGMP-dependent protein kinase.

A:Reference number: S05034; MUID:89325663

A:Accession: S05035

A:Molecule type: mRNA

A:Residues: 1-293 <WER>

A:Cross-references: EMBL:X54289; NID:g213; PIDN:CAA38184.1; PID:g214

R:Wolfe, L.; Francis, S.H.; Corbin, J.D.

J. Biol. Chem. 264, 4157-4162, 1989

A:Title: Properties of a cGMP-dependent monomeric protein kinase from bovine aorta.

A:Reference number: A32952; MUID:89139489

A:Accession: A32952

A:Molecule type: protein

A:Residues: 'E', 64-75 <WOL>

A:Experimental source: aortic smooth muscle

A:Note: monomeric form apparently produced by proteolysis during purification

R:Francis, S.H.; Woodford, T.A.; Wolfe, L.; Corbin, J.D.

Second Messengers Phosphoproteins 12, 301-310, 1989

A:Title: Types Ialpha and Ibeta isozymes of cGMP-dependent protein kinase: alternative m

A:Reference number: A60180

A:Accession: A60180

A:Molecule type: protein

A:Residues: 63-92, 'X', 94, 'X', 219-223, 'X', 225-227, 'XX', 230-255; 294-323 <PRA>

C:Superfamily: cGMP-dependent protein kinase; cAMP receptor protein cyclic nucleotide-bi

C:Keywords: acetylated amino end; alternative splicing; Anp; autophosphorylation; cGMP b

F:118-235/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP1>

F:236-293/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology (fragm

F:2/Modified site: acetylated amino end (Gly) (In mature form) #status predicted
 F:80/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predic

Query Match 74.4% Score 32; DB 2; Length 323;
 Best Local Similarity 66.7%; Pred. No. 38;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KIFGSLAF 9

::|||::||

DB 179 KVFGE LAIL 187

Search completed: November 14, 2000, 11:55:59
 Job time: 77 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 14, 2000, 11:54:42 ; Search time 8.66 Seconds
(without alignments)
33.202 Million cell updates/sec

Title: US-09-277-074-10
Perfect score: 43
Sequence: 1 KIFGSLAFL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 87993 seqs, 31947931 residues

Total number of hits satisfying chosen parameters: 87993

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	100.0	1254	1 ERB2_MESAU	O60553 mesocricetu
2	43	100.0	1255	1 ERB2_HUMAN	P04626 homo sapien
3	43	100.0	1257	1 ERB2_RAT	P06494 rattus norv
4	34	79.1	298	1 RT03_ACACA	P46754 acanthamoeb
5	34	79.1	540	1 YFE0_YEAST	P43562 saccharomyc
6	32	74.4	298	1 NULM_ARTSF	Q37714 artemia san
7	32	74.4	502	1 VL2_HPV48	O80925 human papil
8	32	74.4	670	1 KGPA_BOVIN	P00516 bos taurus
9	32	74.4	670	1 KGPA_HUMAN	Q13976 homo sapien
10	32	74.4	670	1 KGPA_RABIT	O77676 oryctolagus
11	32	74.4	686	1 KGPB_BOVIN	P21136 bos taurus
12	32	74.4	686	1 KGPB_HUMAN	P14619 homo sapien
13	32	74.4	686	1 KGPB_MOUSE	Q92020 mus musculu
14	32	74.4	758	1 YA93_SCHPO	Q09782 schizosacch
15	32	74.4	1029	1 YFC5_YEAST	P43571 saccharomyc
16	31	72.1	206	1 RHTB_ECOLI	P27847 escherichia
17	31	72.1	240	1 YD37_MYCTU	Q10647 mycobacteri
18	31	72.1	251	1 YD37_MYCLE	P51426 mycobacteri
19	31	72.1	573	1 ALPI_YEAST	P38971 saccharomyc
20	31	72.1	678	1 C1CL_RABIT	P51804 oryctolagus
21	31	72.1	687	1 C1CL_HUMAN	P51800 homo sapien
22	31	72.1	687	1 C1CK_RABIT	P51803 oryctolagus
23	31	72.1	687	1 C1CK_RAT	Q06393 rattus norv
24	31	72.1	687	1 C1CL_HUMAN	P51801 homo sapien
25	31	72.1	956	1 CB3L_YEAST	P32504 saccharomyc
26	30	69.8	120	1 MSLC_STAAR	Q68285 staphylococ
27	30	69.8	125	1 DIVC_BACSU	P37471 bacillus su
28	30	69.8	184	1 ADML_MOUSE	P97297 mus musculu
29	30	69.8	242	1 Y252_MYCPN	P75424 mycoplasma
30	30	69.8	284	1 COX3_LEITA	P14546 leishmania
31	30	69.8	348	1 UN97_CAEEL	P50464 caenorhabdi
32	30	69.8	351	1 OM32_COMAC	P24305 comamonas a
33	30	69.8	399	1 YWBF_BACSU	P39589 bacillus su

ALIGNMENTS

```

RESULT_1
ERB2_MESAU
ID   ERB2_MESAU          STANDARD;          PRT;  1254 AA.
AC   Q60553;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   01-OCT-2000 (Rel. 40, Last annotation update)
DE   ERBB-2 RECEPTOR PROTEIN-TYROSINE KINASE PRECURSOR (EC 2.7.1.112)
DE   (P185ERBB2) (NEU PROTO-ONCOGENE).
GN   ERBB2 OR NEU.
OS   Mesocricetus auratus (Golden hamster).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC   Mesocricetus.
RN   [1]
RP   SEQUENCE FROM N.A.
RT   TISSUE=NERVE;
RX   MEDLINE; 94193007.
RA   Nakamura T., Ushijima T., Ishizaka Y., Nagao M., Arai M.,
RA   Yamazaki Y., Ishikawa T.;
RT   *Cloning and activation of the Syrian hamster neu proto-oncogene.*;
RL   Gene 140:251-255(1994).
CC   -!- FUNCTION: ESSENTIAL COMPONENT OF A NEUREGULIN-RECEPTOR COMPLEX,
CC   ALTHOUGH NEUREGULINS DO NOT INTERACT WITH IT ALONE. GP30 IS A
CC   POTENTIAL LIGAND FOR THIS RECEPTOR. NOT ACTIVATED BY EGF, TGF-
CC   ALPHA AND AMPHIREGULIN (BY SIMILARITY).
CC   -!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE -> ADP +
CC   PROTEIN TYROSINE PHOSPHATE.
CC   -!- SUBUNIT: HETERODIMER WITH EACH OF THE OTHER ERBB RECEPTORS
CC   (POTENTIAL).
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE
CC   RESIDUES.
CC   -!- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
CC   -----
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CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----
CC   EMBL; D16295; BAA03801.1; -
CC   DR   INTERPRO; IPR0000494; -
CC   DR   INTERPRO; IPR000719; -
CC   DR   INTERPRO; IPR001245; -
CC   DR   INTERPRO; IPR002174; -
CC   PFAM; PF00757; Furin-like; 1.
CC   PFAM; PF01030; Recep_L_domain; 2.
CC   PFAM; PF00069; pkinase; 1.
CC   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
CC   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
CC   TRANSFAM; Glycoprotein; Multigene family; Receptor; Signal;
CC   Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
KW

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```

34 30 69.8 592 1 TAT2_YEAST
35 30 69.8 779 1 LEU2_YEAST
36 30 69.8 821 1 SYI_THETH
37 30 69.8 963 1 CHS2_YEAST
38 29 67.4 128 1 EFG_PLARO
39 29 67.4 174 1 CHCB_BOMMO
40 29 67.4 179 1 YEH6_YEAST
41 29 67.4 184 1 YPS2_SYNP2
42 29 67.4 186 1 NIAM_HUMAN
43 29 67.4 242 1 CD8A_BOVIN
44 29 67.4 244 1 ERMG_BACSH
45 29 67.4 265 1 BEX1_HAEIN

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p38967 saccharomyc
p07264 saccharomyc
p56690 thermus aqu
p14180 saccharomyc
p72230 planobispor
p08830 bombyx mori
p39979 saccharomyc
p31526 synechoccc
p095169 homo sapien
p31783 bos taurus
p06571 bacillus sp
p19390 haemophilus

```

KW Proto-oncogene; Disease mutation.
 FT SIGNAL 1 21 POTENTIAL.
 FT CHAIN 22 1254 ERBB-2 RECEPTOR PROTEIN-TYROSINE KINASE.
 FT DOMAIN 22 652 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 653 675 POTENTIAL.
 FT DOMAIN 676 1254 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 158 368 CYS-RICH.
 FT DOMAIN 472 644 CYS-RICH.
 FT DOMAIN 720 987 PROTEIN KINASE.
 FT NP_BIND 726 734 ATP (BY SIMILARITY).
 FT BINDING 753 753 ATP (BY SIMILARITY).
 FT ACT_SITE 845 845 BY SIMILARITY.
 FT VARIANT 658 658 V -> E (IN ONCOGENIC NEU).
 FT VARIANT 659 659 V -> E (IN ONCOGENIC NEU).
 FT MOD_RES 1139 1139 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT MOD_RES 1247 1247 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT CARBOHYD 68 68 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 125 125 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 187 187 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 259 259 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 530 530 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 571 571 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 629 629 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 1254 AA; 138252 MW; 974C3791C21F2BE1 CRC64;

Query Match 100.0%; Score 43; DB 1; Length 1254;
 Best Local Similarity 100.0%; Pred. No. 0.39;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIFGSIAFL 9
 |||||
 DB 369 KIFGSIAFL 377

RESULT 2
 ERB2_HUMAN STANDARD; PRT: 1255 AA.
 AC P04626;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE RECEPTOR PROTEIN-TYROSINE KINASE ERBB-2 PRECURSOR (EC 2.7.1.112)
 DE (P185ERBB2) (NEU PROTO-ONCOGENE) (C-ERBB-2) (TYROSINE KINASE-TYPE CELL
 DE SURFACE RECEPTOR HER2) (MLN 19).
 DE ERBB2 OR HER2 OR NGL OR NEU.
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 86118663.
 RA Yamamoto T., Ikawa S., Akiyama T., Semba K., Nomura N., Miyajima N.,
 RA Saito T., Toyoshima K.;
 RA "Similarity of protein encoded by the human c-erb-B-2 gene to
 RT epidermal growth factor receptor.";
 RL Nature 319:230-234(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 86070181.
 RA Coussens L., Yang-Feng T.L., Liao Y.C., Chen E., Gray A.,
 RA McGrath J., Seeburg P.H., Libermann T.A., Schlessinger J.,
 RA Francke U., Levinson A., Ullrich A.;
 RT "Tyrosine kinase receptor with extensive homology to EGF receptor
 RT shares chromosomal location with neu oncogene.";
 RL Science 230:1132-1139(1985).
 RN [3]
 RP SEQUENCE OF 737-1031 FROM N.A.
 RX MEDLINE; 86016729.
 RA Semba K., Kamata N., Toyoshima K., Yamamoto T.;
 RT "A v-erbB-related protooncogene, c-erbB-2, is distinct from the
 RT c-erbB-1/epidermal growth factor-receptor gene and is amplified in a
 RT human salivary gland adenocarcinoma.";

Proc. Natl. Acad. Sci. U.S.A. 82:6497-6501(1985).
 [4]
 RL VARIANTS VAL-654 AND VAL-655.
 RN MEDLINE; 93194196.
 RX Ehsani A., Low J., Wallace R.B., Wu A.M.;
 RA "Characterization of a new allele of the human ERBB2 gene by allele-
 RT specific competition hybridization.";
 RL Genomics 15:426-429(1993).
 CC -1- FUNCTION: ESSENTIAL COMPONENT OF A NEUREGULIN-RECEPTOR COMPLEX,
 CC ALTHOUGH NEUREGULINS DO NOT INTERACT WITH IT ALONE. GP30 IS A
 CC POTENTIAL LIGAND FOR THIS RECEPTOR. NOT ACTIVATED BY EGF, TGF-
 CC ALPHA AND AMPHIREGULIN.
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
 CC PROTEIN TYROSINE PHOSPHATE.
 CC -1- SUBUNIT: HETERODIMER WITH EACH OF THE OTHER ERBB RECEPTORS
 CC (POTENTIAL).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE
 CC RESIDUES (BY SIMILARITY).
 CC -1- POLYMORPHISM: THERE ARE FOUR ALLELES DUE TO THE VARIATIONS IN
 CC POSITIONS 654 AND 655. ALLELE B1 (654-ILE-655) HAS A FREQUENCY
 CC OF 0.782; ALLELE B2 (654-ILE-VAL-655) HAS A FREQUENCY OF 0.206;
 CC ALLELE B3 (654-VAL-VAL-655) HAS A FREQUENCY OF 0.012.
 CC -1- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
 CC -----
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 CC -----
 DR EMBL; M11767; AAA35808.1;
 DR EMBL; M11761; AAA35808.1; JOINED.
 DR EMBL; M11762; AAA35808.1; JOINED.
 DR EMBL; M11763; AAA35808.1; JOINED.
 DR EMBL; M11764; AAA35808.1; JOINED.
 DR EMBL; M11765; AAA35808.1; JOINED.
 DR EMBL; M11766; AAA35808.1; JOINED.
 DR EMBL; M11730; AAA75493.1;
 DR EMBL; M12036; AAA35978.1;
 DR EMBL; X03363; CAA27060.1;
 DR PIR; A25491; A25491.
 DR PIR; A24571; A24571.
 DR HSP; P11362; 1FGI.
 DR MIM; 164870;
 DR INTERPRO; IPR000494;
 DR INTERPRO; IPR000719;
 DR INTERPRO; IPR001245;
 DR INTERPRO; IPR002174;
 DR PFAM; PF00757; Furin-like; 1.
 DR PFAM; PF01030; Recep_L-domain; 2.
 DR PFAM; PF00069; pkinase; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 KW Transmembrane; Glycoprotein; Multigene family; Receptor; Signal;
 KW Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 KW Polymorphism.
 FT SIGNAL 1 21 POTENTIAL.
 FT CHAIN 22 1255 RECEPTOR PROTEIN-TYROSINE KINASE ERBB-2.
 FT DOMAIN 22 652 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 653 675 POTENTIAL.
 FT DOMAIN 676 1255 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 720 987 PROTEIN KINASE.
 FT NP_BIND 726 734 ATP (BY SIMILARITY).
 FT BINDING 753 753 ATP (BY SIMILARITY).
 FT ACT_SITE 845 845 BY SIMILARITY.
 FT MOD_RES 1139 1139 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT MOD_RES 1248 1248 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT CARBOHYD 68 68 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 124 124 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 187 187 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 259 259 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 530 530 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 571 571 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 629 629 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 654 654 I -> V.
FT VARIANT 655 655 /FTID=VAR_004077.
FT VARIANT 655 655 I -> V.
FT CONFLICT 1170 1170 /FTID=VAR_004078.
FT CONFLICT 1170 1170 P -> A (IN REF. 2).
SQ SEQUENCE 1255 AA; 137909 MW; 39E9DFA04DCF962 CRC64;

Query Match 100.0%; Score 43; DB 1; Length 1257;
Best Local Similarity 100.0%; Pred. NO. 0.39;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIFGSLAFL 9
Db 369 KIFGSLAFL 377
|||||

RESULT 3
ERR2_RAT
ID ERR2_RAT STANDARD; PRT; 1257 AA.
AC P06494;
DT 01-JAN-1988 (Rel. 06, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE 01-OCT-2000 (Rel. 40, Last annotation update)
DE ERBB-2 RECEPTOR PROTEIN-TYROSINE KINASE PRECURSOR (EC 2.7.1.112)
DE (P185ERBB2) (NEU PROTO-ONCOGENE) (EPIDERMAL GROWTH FACTOR RECEPTOR-RELATED PROTEIN).
DE ERBB2 OR NEU.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
[1]
RN SEQUENCE FROM N.A.
RP TISSUE-NEUROBLASTOMA;
RX MEDLINE; 86118662.
RA Bargmann C.I., Hung M.-C., Weinberg R.A.;
RT "The neu oncogene encodes an epidermal growth factor receptor-related protein.;"
RL Nature 319:226-230(1986).
[2]
RN SEQUENCE OF 852-905 FROM N.A.
RP TISSUE-SCIATIC NERVE;
RX MEDLINE; 91222560.
RA Lai C., Lemke G.;
RT "An extended family of protein-tyrosine kinase genes differentially expressed in the vertebrate nervous system.;"
RL Neuron 6:691-704(1991).
[3]
RP STRUCTURE BY NMR OF 650-668.
RX MEDLINE; 92155181.
RA Guillek W.J., Bottomley A.C., Lofts F.J., Doak D.G., Mulvey D.,
RA Newman R., Crumpton M.J., Sternberg M.J.E., Campbell I.D.;
RT "Three dimensional structure of the transmembrane region of the proto-oncogenic and oncogenic forms of the neu protein.;"
RL EMBO J. 11:43-48(1992).
CC -1- FUNCTION: ESSENTIAL COMPONENT OF A NEUREGULIN-RECEPTOR COMPLEX, ALTHOUGH NEUREGULINS DO NOT INTERACT WITH IT ALONE. GP30 IS A POTENTIAL LIGAND FOR THIS RECEPTOR. NOT ACTIVATED BY EGF, TGF-ALPHA AND AMPHIREGULIN.
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN TYROSINE PHOSPHATE.
CC -1- SUBUNIT: HETERODIMER WITH EACH OF THE OTHER ERBB RECEPTORS. THE CONSTITUTIVELY ACTIVATED ONCOGENIC VARIANT FORMS A HOMODIMER.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE RESIDUES (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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CC -----
CC EMBL; X03362; CAA27059.1; ALT_INIT.
DR PIR; A24562; TVRTNU.
DR HSP; P11362; IFGI.
DR INTERPRO; IPR000494; .
DR INTERPRO; IPR000719; .
DR INTERPRO; IPR001245; .
DR INTERPRO; IPR002174; .
DR PFAM; PF00757; Furin-like; 1.
DR PFAM; PF01030; Recep_L-domain; 2.
DR PFAM; PF00069; kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW Transmembrane; Glycoprotein; Multigene family; Receptor; Signal;
KW Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
KW Proto-oncogene; Disease mutation.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 1257 ERBB-2 RECEPTOR PROTEIN-TYROSINE KINASE.
FT DOMAIN 22 654 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 655 677 POTENTIAL.
FT DOMAIN 678 1257 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 159 369 CYS-RICH.
FT DOMAIN 473 646 CYS-RICH.
FT DOMAIN 722 989 PROTEIN KINASE.
FT NP_BIND 728 736 ATP (BY SIMILARITY).
FT BINDING 755 755 ATP (BY SIMILARITY).
FT ACT_SITE 847 847 BY SIMILARITY.
FT VARIANT 661 661 V -> E (IN ONCOGENIC NEU).
FT MOD_RES 1141 1141 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 1250 1250 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CARBOHYD 68 68 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 532 532 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 573 573 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 631 631 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1257 AA; 138831 MW; 6129264583011402 CRC64;

Query Match 100.0%; Score 43; DB 1; Length 1257;
Best Local Similarity 100.0%; Pred. NO. 0.39;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIFGSLAFL 9
Db 370 KIFGSLAFL 378
|||||

RESULT 4
RT03_ACACA
ID RT03_ACACA STANDARD; PRT; 298 AA.
AC P46754;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE MITOCHONDRIAL RIBOSOMAL PROTEIN S3.
GN RPS3.
OS Acanthamoeba castellanii (Amoeba).
OC Mitochondrion.
OC Eukaryota; Acanthamoebidae; Acanthamoeba.
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 30010 / NEFF;
RX MEDLINE; 95147275.
RA Burger G., Plante I., Loneragan K.M., Gray M.W.;

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RT The mitochondrial DNA of the amoeboid protozoan, Acanthamoeba
 RT castellanii: complete sequence, gene content and genome
 RT organization.";
 RL J. Mol. Biol. 245:522-537(1995).
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL.
 CC -1- SIMILARITY: BELONGS TO THE S3P FAMILY OF RIBOSOMAL PROTEINS.
 CC -----
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 CC -----
 DR EMBL: U12386; AAD11841.1; -;
 DR INTERPRO: IPR001351; -;
 DR PFAM: PF00189; Ribosomal_S3_C; 1;
 DR PFAM: PF00417; Ribosomal_S3_N; 1;
 DR PROSITE: PS00548; RIBOSOMAL_S3; FALSE_NEG.
 KW Ribosomal protein; Mitochondrion.
 SQ SEQUENCE 298 AA; 36060 MW; 29415935EE187DE6 CRC64;

Query Match 79.1%; Score 34; DB 1; Length 298;
 Best Local Similarity 87.5%; Pred. No. 7.3;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KIFGSLAF 8

DB 250 KAFGSLAF 257

RESULT 5

YFEO_YEAST
 ID YFEO_YEAST STANDARD; PRT; 540 AA.
 AC P43562;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE PROBABLE METABOLITE TRANSPORT PROTEIN YFEO40W.
 GN YFEO40W.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 OC Saccharomycetaceae; Saccharomycetes.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C / AB972;
 RX MEDLINE: 93400292.
 RA Murakami Y., Naitou M., Hagiwara H., Shibata T., Ozawa M.,
 RA Sasanuma S.-I., Sasanuma M., Tsuchiya Y., Soeda E., Yokoyama K.,
 RA Yamazaki M., Tashiro H., Eki T.;
 RT "Analysis of the nucleotide sequence of chromosome VI from
 RT Saccharomyces cerevisiae";
 RL Nat. Genet. 10:261-268(1995).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE).
 CC -1- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
 CC -----
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 CC -----
 DR EMBL: D50617; BAA09200.1; -;
 DR EMBL: D44598; BAA08025.1; -;
 DR SGD: S0001854; YFEO40W.
 DR INTERPRO: IPR001066; -;
 DR PFAM: PF00083; sugar_tr; 1;
 DR PROSITE: PS00216; SUGAR_TRANSPORT_1; FALSE_NEG.
 DR PROSITE: PS00217; SUGAR_TRANSPORT_2; 1.

KW Hypothetical protein; Repeat; Transport; Transmembrane.
 FT TRANSMEM 30 50
 FT TRANSMEM 68 88
 FT TRANSMEM 102 122
 FT TRANSMEM 127 147
 FT TRANSMEM 159 179
 FT TRANSMEM 188 208
 FT TRANSMEM 276 296
 FT TRANSMEM 314 334
 FT TRANSMEM 342 362
 FT TRANSMEM 386 406
 FT TRANSMEM 429 449
 FT TRANSMEM 456 476
 SQ SEQUENCE 540 AA; 60610 MW; A43B6B58134C38AE CRC64;

Query Match 79.1%; Score 34; DB 1; Length 540;
 Best Local Similarity 87.5%; Pred. No. 13;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 IFGSLAFL 9

DB 459 IFGSLTFL 466

RESULT 6

NUIM_ARTSF
 ID NUIM_ARTSF STANDARD; PRT; 298 AA.
 AC Q37714;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1 (EC 1.6.5.3).
 GN ND1 OR ND-1
 OS Artemia sanfranciscana (Brine shrimp) (Artemia franciscana).
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Branchiopoda; Anostraca;
 OC Artemiidae; Artemia.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 94223692.
 RA Perez M.L., Valverde J.R., Batuecas B., Amat F., Marco R., Garesse R.;
 RT "Speciation in the Artemia genus: mitochondrial DNA analysis of
 RT bisexual and parthenogenetic brine shrimps.";
 RL J. Mol. Evol. 38:156-168(1994).
 CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE -> NAD(+) + UBIQUINOL.
 CC -1- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 1 FAMILY.
 CC -----
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 CC -----
 DR EMBL: X69067; CAA48818.1; -;
 DR INTERPRO: IPR001694; -;
 DR PFAM: PF00146; NADhdh; 1;
 DR PROSITE: PS00667; COMPLEX1_ND1_1; 1;
 DR PROSITE: PS00668; COMPLEX1_ND1_2; 1;
 KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Transmembrane.
 SQ SEQUENCE 298 AA; 33763 MW; 07FED8CD6219E11E CRC64;

Query Match 74.4%; Score 32; DB 1; Length 298;
 Best Local Similarity 62.5%; Pred. No. 19;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 IFGSLAFL 9

DB 241 VFGSWSFL 248

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RESULT 7
VL2_HP48
ID VL2_HP48 STANDARD; PRT; 502 AA.
AC Q80925;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE MINOR CAPSID PROTEIN L2.
GN L2.
OS Human papillomavirus type 48.
OC Viruses; dsDNA viruses, no RNA stage; Papovaviridae; Papillomavirus.
RN [1]
RP SEQUENCE FROM N.A.
RA Delius H.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
DR EMBL; U31789; AAA79469.1; -.
DR INTERPRO; IPR000784; -.
DR PFAM; PF00513; Late_protein_L2; 1.
KW Coat protein; Late protein.
SQ SEQUENCE 502 AA; 54435 MW; C42DE45A7E73EE29 CRC64;

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Query Match 74.4%; Score 32; DB 1; Length 502;
Best Local Similarity 75.0%; Pred. No. 32;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 KIFGSLAF 8
| | | | |
Db 43 KIFGSLVY 50

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RESULT 8
KQPA_BOVIN
ID KQPA_BOVIN STANDARD; PRT; 670 AA.
AC P00516;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CGMP-DEPENDENT PROTEIN KINASE 1, ALPHA ISOZYME (EC 2.7.1.37) (CGK 1
DE ALPHA) (CGK1-ALPHA).
GN PRKG1 OR PRKG1A.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89325663.
RA Wernet W., Flockerzi V., Hofmann F.;
RT "The cDNA of the two isoforms of bovine cGMP-dependent protein
RT kinase."
RL FEBS Lett. 251:191-196(1989).
RN [2]
RP SEQUENCE OF 1-17; 89-374 AND 407-670.
RX MEDLINE; 85023307.
RA Takio K., Wade R.D., Smith S.B., Krebs E.G., Walsh K.A., Titani K.;
RT "Guanosine cyclic 3',5'-phosphate dependent protein kinase, a
RT chimeric protein homologous with two separate protein families."
RL Biochemistry 23:4207-4218(1984).
RN [3]
RP SEQUENCE OF 13-104.
RX MEDLINE; 83213511.
RA Takio K., Smith S.B., Walsh K.A., Krebs E.G., Titani K.;

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RT "Amino acid sequence around a 'hinge' region and its
RT 'autophosphorylation' site in bovine Lung cGMP-dependent protein
RT kinase."
RL J. Biol. Chem. 258:5531-5536(1983).
RN [4]
RP SEQUENCE OF 373-409.
RX MEDLINE; 82098123.
RA Hashimoto E., Takio K., Krebs E.G.;
RT "Amino acid sequence at the ATP-binding site of cGMP-dependent
RT protein kinase."
RL J. Biol. Chem. 257:727-733(1982).
CC -|- CATALYTIC ACTIVITY: ATP + A PROTEIN -> ADP + A PHOSPHOPROTEIN.
CC -|- ENZYME REGULATION: BINDING OF CGMP TO CGK RESULTS IN ENZYME
CC ACTIVATION.
CC -|- SUBUNIT: ANTIPARALLEL HOMODIMER.
CC -|- ALTERNATIVE PRODUCTS: 2 ISOFORMS; CGK1-ALPHA (SHOWN HERE) AND
CC CGK1-BETA (P21136); ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -|- MISCELLANEOUS: EXHIBIT A SUBSTRATE SPECIFICITY SIMILAR BUT NOT
CC IDENTICAL TO THAT OF CAK.
CC -|- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CGMP SUBFAMILY.
CC -|- SIMILARITY: CONTAINS 2 CYCLIC NUCLEOTIDE-BINDING DOMAINS.
CC -----
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CC -----
DR EMBL; X16086; CAA34214.1; -.
DR PIR; A00619; OKBOG.
DR PIR; S05034; S05034.
DR HSP; P05132; 20PK.
DR INTERPRO; IPR000595; -.
DR INTERPRO; IPR000719; -.
DR INTERPRO; IPR000961; -.
DR INTERPRO; IPR002290; -.
DR INTERPRO; IPR002374; -.
DR PFAM; PF00027; cGMP_binding; 2.
DR PFAM; PF00069; pkinase; 1.
DR PFAM; PF00433; pkinase_C; 1.
DR PRINTS; PR00104; CGMPKINASE.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00888; CNMP_BINDING_1; 2.
DR PROSITE; PS00889; CNMP_BINDING_2; 2.
DR PROSITE; PS00042; CNMP_BINDING_3; 2.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW CGMP-binding; Acetylation; Phosphorylation; Alternative splicing.
FT INIT_MET 0 0
FT MOD_RES 1 1 ACETYLATION.
FT DISULFID 42 42 INTERCHAIN (WITH DIMER).
FT MOD_RES 58 58 PHOSPHORYLATION (AUTO-).
FT DOMAIN 1 101 DIMERIZATION.
FT NP_BIND 102 219 CGMP 1.
FT NP_BIND 220 340 CGMP 2.
FT DOMAIN 359 618 PROTEIN KINASE.
FT NP_BIND 365 373 ATP (BY SIMILARITY).
FT BINDING 389 389 ATP (BY SIMILARITY).
FT ACT_SITE 483 483 BY SIMILARITY.
SQ SEQUENCE 670 AA; 76287 MW; A8E37ACFE8A7557D CRC64;

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Query Match 74.4%; Score 32; DB 1; Length 670;
Best Local Similarity 66.7%; Pred. No. 42;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KIFGSLAF 9
| | | | |
Db 163 KVFGE LAIL 171

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RESULT 9
KGPA_HUMAN STANDARD; PRT; 670 AA.
AC Q13976;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE CMMP-DEPENDENT PROTEIN KINASE 1, ALPHA ISOZYME (EC 2.7.1.37) (CGK 1
DE ALPHA) (CGKI-ALPHA).
GN PRKG1 OR PRKG1A.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RX MEDLINE; 96188981.
RA Tamura N., Itoh H., Ogawa Y., Nakagawa O., Harada M., Chun T.,
RA Suga S., Yoshimasa T., Nakao K.;
RT "cDNA cloning and gene expression of human type IaIpha cGMP-dependent
RT protein kinase.";
RL Hypertension 27:552-557(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97336057.
RA Orstavik S., Natarajan V., Tasken K., Jahnsen T., Sandberg M.;
RT "Characterization of the human gene encoding the type I alpha and
RT type I beta cGMP-dependent protein kinase (PRKG1).";
RL Genomics 42:311-318(1997).
CC -!- CATALYTIC ACTIVITY: ATP + A PROTEIN = ADP + A PHOSPHOPROTEIN.
CC -!- ENZYME REGULATION: BINDING OF CGMP TO CGK RESULTS IN ENZYME
CC ACTIVATION (BY SIMILARITY).
CC -!- SUBUNIT: ANTIPARALLEL HOMODIMER (BY SIMILARITY).
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; CGKI-ALPHA (SHOWN HERE) AND
CC CGKI-BETA (P14619); ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- MISCELLANEOUS: EXHIBIT A SUBSTRATE SPECIFICITY SIMILAR BUT NOT
CC IDENTICAL TO THAT OF CAK (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CGMP SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 2 CYCLIC NUCLEOTIDE-BINDING DOMAINS.
CC
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CC
CC EMBL; 292867; CAB07436.1; JOINED.
CC EMBL; 292869; CAB07436.1; JOINED.
CC EMBL; 292870; CAB07436.1; JOINED.
CC EMBL; 292871; CAB07436.1; JOINED.
CC EMBL; 292872; CAB07436.1; JOINED.
CC EMBL; 292873; CAB07436.1; JOINED.
CC EMBL; 292874; CAB07436.1; JOINED.
CC EMBL; 292875; CAB07436.1; JOINED.
CC EMBL; 292876; CAB07436.1; JOINED.
CC EMBL; 292877; CAB07436.1; JOINED.
CC EMBL; 292878; CAB07436.1; JOINED.
CC EMBL; 292879; CAB07436.1; JOINED.
CC EMBL; 292880; CAB07436.1; JOINED.
CC EMBL; 292881; CAB07436.1; JOINED.
CC EMBL; 292882; CAB07436.1; JOINED.
CC EMBL; 292883; CAB07436.1; JOINED.
CC EMBL; 292884; CAB07436.1; JOINED.
CC EMBL; 292885; CAB07436.1; JOINED.
CC EMBL; D45864; BAA08297.1; JOINED.
CC MIM; 176894;
CC INTERPRO: IPR000595;
CC INTERPRO: IPR000719;

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DR INTERPRO: IPR000961;
DR INTERPRO: IPR001245;
DR INTERPRO: IPR002290;
DR INTERPRO: IPR002373;
DR INTERPRO: IPR002374;
DR PFAM: PF00027; CNMP_binding; 2.
DR PFAM: PF00069; kinase; 1.
DR PFAM: PF00433; kinase_C; 1.
DR PRINTS: PR00103; CAMPKINASE.
DR PRINTS: PR00104; CGMPKINASE.
DR PRINTS: PR00109; TYRKINASE.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00888; CNMP_BINDING_1; 2.
DR PROSITE: PS00889; CNMP_BINDING_2; 2.
DR PROSITE: PS00892; CNMP_BINDING_3; 2.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW CGMP-binding; Acetylation; Phosphorylation; Alternative splicing.
FT INIT_MET 0 0 BY SIMILARITY.
FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
FT DISULFID 42 42 INTERCHAIN (WITH DIMER) (BY SIMILARITY).
FT MOD_RES 58 58 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT DOMAIN 1 101 DIMERIZATION (BY SIMILARITY).
FT NP_BIND 102 219 CGMP 1.
FT NP_BIND 220 340 CGMP 2.
FT DOMAIN 359 618 PROTEIN KINASE.
FT NP_BIND 365 373 ATP (BY SIMILARITY).
FT BINDING 389 389 ATP (BY SIMILARITY).
FT ACT_SITE 483 483 BY SIMILARITY.
SQ SEQUENCE 670 AA; 76233 MW; 663C4B496F983270 CRC64;

Query Match 74.4%; Score 32; DB 1; Length 670;
Best Local Similarity 66.7%; Pred. No. 42;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KIFGSLAFL 9
   :|||
DB 163 KVFGEALAIL 171

RESULT 10
KGPA_RABBIT STANDARD; PRT; 670 AA.
AC Q77676;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CGMP-DEPENDENT PROTEIN KINASE 1, ALPHA ISOZYME (EC 2.7.1.37) (CGK 1
DE ALPHA) (CGKI-ALPHA).
GN PRKG1.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NEW ZEALAND WHITE; TISSUE=HEART;
RA Kumar R., Joyner R.W., Lincoln T.W.;
RT "cDNA cloning and analysis of expression of cGMP-dependent protein
RT kinase in rabbit heart.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: ATP + A PROTEIN = ADP + A PHOSPHOPROTEIN.
CC -!- ENZYME REGULATION: BINDING OF CGMP TO CGK RESULTS IN ENZYME
CC ACTIVATION (BY SIMILARITY).
CC -!- SUBUNIT: ANTIPARALLEL HOMODIMER (BY SIMILARITY).
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; CGKI-ALPHA (SHOWN HERE) AND
CC CGKI-BETA; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- MISCELLANEOUS: EXHIBIT A SUBSTRATE SPECIFICITY SIMILAR BUT NOT
CC IDENTICAL TO THAT OF CAK (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -!- CGMP SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 2 CYCLIC NUCLEOTIDE-BINDING DOMAINS.
CC

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-----
CC EMBL: AF076969; AAC31192.1; -
CC INTERPRO: IPR000595; -
CC INTERPRO: IPR000719; -
CC INTERPRO: IPR000961; -
CC INTERPRO: IPR001245; -
CC INTERPRO: IPR002290; -
CC INTERPRO: IPR002373; -
CC INTERPRO: IPR002374; -
CC PFAM: PF00027; CNMP_binding; 2.
CC PFAM: PF00069; pkinase; 1.
CC PRINTS: PR00103; CAMPKINASE.
CC PRINTS: PR00104; CGMPKINASE.
CC PRINTS: PR00109; TYRKINASE.
CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
CC PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
CC PROSITE: PS00888; CNMP_BINDING_1; 2.
CC PROSITE: PS00889; CNMP_BINDING_2; 2.
CC PROSITE: PS00042; CNMP_BINDING_3; 2.
CC Transferase; Serine/threonine-protein kinase; ATP-binding;
CC CNMP-binding; Acetylation; Phosphorylation; Alternative splicing.
CC INIT_MET 0 0
CC MOD_RES 1 1
CC DISULFID 42 42
CC MOD_RES 58 58
CC DOMAIN 1 101
CC NP_BIND 102 219
CC NP_BIND 220 340
CC DOMAIN 359 618
CC NP_BIND 365 373
CC BINDING 389 389
CC ACT_SITE 483 483
CC VARIANT 557 557
CC SEQUENCE 670 AA; 76322 MW; CFEID7D939EIC423 CRC64;

Query Match 74.4% Score 32; DB 1; Length 670;
Best Local Similarity 66.7%; Pred.No. 42; Indels 0; Gaps 0;
Matches 6; Conservative 1; Mismatches 2;

Qy 1 KIFGSLAFL 9
Db 163 KVFGEALAIL 171

RESULT 11
KGPB_BOVIN STANDARD; PRT; 686 AA.
AC P21136;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE CMMP-DEPENDENT PROTEIN KINASE 1, BETA ISOZYME (EC 2.7.1.37) (CGK 1
DE BETA) (CGKI-BETA).
GN PRKG1 OR PRKG1B OR PRKG1C.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
RN 11)
RP SEQUENCE FROM N.A.
RC TISSUE-TESTIS;
RX MEDLINE; 97256767.

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RA Ruth P., Pfeifer A., Kamm S., Klatt P., Dostmann W.R., Hofmann F.;
RA "Identification of the amino acid sequences responsible for high
RT affinity activation of cGMP kinase Ialpha.";
RL J. Biol. Chem. 272:10522-10528(1997).
RN [2]
RP SEQUENCE OF 1-293 FROM N.A.
RC TISSUE=TRACHEA SMOOTH MUSCLE;
RX MEDLINE; 89325663.
RA Wernet W., Flockerzi V., Hofmann F.;
RT "The cDNA of the two isoforms of bovine cGMP-dependent protein
RT kinase.";
RL FEBS Lett. 251:191-196(1989).
CC -|- CATALYTIC ACTIVITY: ATP + A PROTEIN = ADP + A PHOSPHOPROTEIN.
CC -|- ENZYME REGULATION: BINDING OF CGMP TO CGK RESULTS IN ENZYME
CC ACTIVATION.
CC -|- SUBUNIT: ANTIPARALLEL HOMODIMER.
CC -|- ALTERNATIVE PRODUCTS: 2 ISOFORMS; CGKI-ALPHA (P00516) AND
CC CGKI-BETA (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -|- MISCELLANEOUS: EXHIBIT A SUBSTRATE SPECIFICITY SIMILAR BUT NOT
CC IDENTICAL TO THAT OF CAK.
CC -|- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CGMP SUBFAMILY.
CC -|- SIMILARITY: CONTAINS 2 CYCLIC NUCLEOTIDE-BINDING DOMAINS.
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-----
CC EMBL: Y08961; CAA70155.1; -
CC EMBL: X54289; CAA38184.1; -
CC PIR: S05035; S05035.
CC HSP: P05132; 2CPK.
CC INTERPRO: IPR000595; -
CC INTERPRO: IPR000719; -
CC INTERPRO: IPR000961; -
CC INTERPRO: IPR002290; -
CC INTERPRO: IPR002374; -
CC PFAM: PF00027; CNMP_binding; 2.
CC PFAM: PF00069; pkinase; 1.
CC PFAM: PF00433; pkinase_C; 1.
CC PRINTS: PR00104; CGMPKINASE.
CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
CC PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
CC PROSITE: PS00888; CNMP_BINDING_1; 2.
CC PROSITE: PS00889; CNMP_BINDING_2; 2.
CC PROSITE: PS00042; CNMP_BINDING_3; 2.
CC Transferase; Serine/threonine-protein kinase; ATP-binding;
CC CNMP-binding; Alternative splicing.
CC NP_BIND 118 235
CC NP_BIND 236 427
CC DOMAIN 375 634
CC FT NP_BIND 381 389
CC FT NP_BIND 405 405
CC FT BINDING 499 499
CC ACT_SITE 499 499
CC BY SIMILARITY.
CC SEQUENCE 686 AA; 77857 MW; 6E48359C35BB96EB CRC64;

Query Match 74.4% Score 32; DB 1; Length 686;
Best Local Similarity 66.7%; Pred.No. 43; Indels 0; Gaps 0;
Matches 6; Conservative 1; Mismatches 2;

Qy 1 KIFGSLAFL 9
Db 179 KVFGEALAIL 187

RESULT 12
KGPB_HUMAN

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ID KGPB_HUMAN STANDARD; PRT; 686 AA.
AC FI4619;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CGMP-DEPENDENT PROTEIN KINASE 1, BETA ISOZYME (EC 2.7.1.37) (CGK 1
DE BETA) (CGKI-BETA).
GN PRKGI OR PRKGRI OR PRKGLB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RX MEDLINE; 90005998.
RA Sandberg M., Natarajan V., Ronander I., Kalderon D., Walter U.,
RA Lohmann S.M., Jahnsen T.;
RT "Molecular cloning and predicted full-length amino acid sequence of
RT the type I beta isozyme of cGMP-dependent protein kinase from human
RT placenta. Tissue distribution and developmental changes in rat.";
RL FEBS Lett. 255:321-329(1989).
RN [2]
RP REVISIONS.
RA Sandberg M.;
RL Submitted (OCT-1989) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97336057.
RA Orstavik S., Natarajan V., Tasken K., Jahnsen T., Sandberg M.;
RT "Characterization of the human gene encoding the type I alpha and
RT type I beta cGMP-dependent protein kinase (PRKGI).";
RL Genomics 42:311-318(1997).
CC -!- CATALYTIC ACTIVITY: ATP + A PROTEIN -> ADP + A PHOSPHOPROTEIN.
CC -!- ENZYME REGULATION: BINDING OF CGMP TO CGK RESULTS IN ENZYME
CC ACTIVATION.
CC -!- SUBUNIT: ANTIPARALLEL HOMODIMER.
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; CGK1-ALPHA (Q13976) AND
CC CGK1-BETA (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- MISCELLANEOUS: EXHIBIT A SUBSTRATE SPECIFICITY SIMILAR BUT NOT
CC IDENTICAL TO THAT OF CAK.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CGMP SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 2 CYCLIC NUCLEOTIDE-BINDING DOMAINS.
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CC -----
CC EMBL; Y07512; CAA68810.1; -
CC EMBL; 292868; CAB07437.1; -
CC EMBL; 292869; CAB07437.1; JOINED.
CC EMBL; 292870; CAB07437.1; JOINED.
CC EMBL; 292871; CAB07437.1; JOINED.
CC EMBL; 292872; CAB07437.1; JOINED.
CC EMBL; 292873; CAB07437.1; JOINED.
CC EMBL; 292874; CAB07437.1; JOINED.
CC EMBL; 292875; CAB07437.1; JOINED.
CC EMBL; 292876; CAB07437.1; JOINED.
CC EMBL; 292877; CAB07437.1; JOINED.
CC EMBL; 292878; CAB07437.1; JOINED.
CC EMBL; 292879; CAB07437.1; JOINED.
CC EMBL; 292880; CAB07437.1; JOINED.
CC EMBL; 292881; CAB07437.1; JOINED.
CC EMBL; 292882; CAB07437.1; JOINED.
CC EMBL; 292883; CAB07437.1; JOINED.
CC EMBL; 292884; CAB07437.1; JOINED.
CC EMBL; 292885; CAB07437.1; JOINED.
CC EMBL; 292886; CAB07437.1; JOINED.
CC EMBL; 292887; CAB07437.1; JOINED.
CC EMBL; 292888; CAB07437.1; JOINED.
CC EMBL; 292889; CAB07437.1; JOINED.
CC EMBL; 292890; CAB07437.1; JOINED.
CC EMBL; 292891; CAB07437.1; JOINED.
CC EMBL; 292892; CAB07437.1; JOINED.
CC EMBL; 292893; CAB07437.1; JOINED.
CC EMBL; 292894; CAB07437.1; JOINED.
CC EMBL; 292895; CAB07437.1; JOINED.
CC EMBL; 292896; CAB07437.1; JOINED.
CC EMBL; 292897; CAB07437.1; JOINED.
CC EMBL; 292898; CAB07437.1; JOINED.
CC EMBL; 292899; CAB07437.1; JOINED.
CC EMBL; 292900; CAB07437.1; JOINED.
CC EMBL; 292901; CAB07437.1; JOINED.
CC EMBL; 292902; CAB07437.1; JOINED.
CC EMBL; 292903; CAB07437.1; JOINED.
CC EMBL; 292904; CAB07437.1; JOINED.
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DR
EMBL: Z54308; CAA91096.1; -.
KW
FT Hypothetical protein; Transmembrane.
TRANSMEM 4 24 POTENTIAL.

FT	TRANSMEM	309	329	POTENTIAL.
FT	TRANSMEM	405	425	POTENTIAL.
FT	TRANSMEM	431	451	POTENTIAL.
FT	TRANSMEM	510	530	POTENTIAL.
FT	TRANSMEM	533	553	POTENTIAL.
FT	TRANSMEM	561	581	POTENTIAL.
FT	TRANSMEM	598	618	POTENTIAL.
FT	TRANSMEM	667	687	POTENTIAL.
FT	TRANSMEM	698	718	POTENTIAL.
FT	TRANSMEM	733	753	POTENTIAL.
SQ	SEQUENCE	758 AA;	85645 MW; F0FE169B570ACC57 CRC64;	

Query Match 74.4%; Score 32; DB 1; Length 758;
Best Local Similarity 66.7%; pred. No. 47;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy	1 KIFGSLAFL 9 : :
Dd	12 QIFGSILFL 20

RESULT 15
YFC5_YEAST
ID YFC5_YEAST STANDARD; PRT; 1029 AA.
AC P43571:
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE DE HYPOTHEITICAL 117.8 KDA PROTEIN IN SPE2-FRS2 INTERGENIC REGION.
GN YFLO25C.

OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomyces.
RN [1]
RP SEQUENCE FROM N.A.

RC STRALIN=S288C / AB972;
RX MEDLINE; 95400292.
RA Murakami Y., Naitou M., Hagiwara H., Shibata T., Ozawa M.,
RA Sasanuma S.-I., Sasanuma M., Tsuchiya Y., Soeda E., Yokoyama K.,

RT "Analysis of the nucleotide sequence of chromosome VI from
 RI *Saccharomyces cerevisiae*.";
 RL Nat. Genet. 10:261-268(1995).
 CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -----
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 CC or send an email to license@isb-sib.ch).
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 CC EMBL; D50617; BAA09213.1; -;
 DR SGD; S0001869; RST1
 DR

KW	Hypothetical protein; Transmembrane.
FT	TRANSMEM 57 POTENTIAL.
FT	TRANSMEM 804 824 POTENTIAL.
FT	TRANSMEM 872 892 POTENTIAL.
FT	TRANSMEM 920 940 POTENTIAL.
FT	TRANSMEM 957 977 POTENTIAL.
FT	TRANSMEM 985 1005 POTENTIAL.
SQ	SEQUENCE 1029 AA; 117754 MW; 10B77B21E5AD686 CRC64;
Query Match 74.4%; Score 32; DB 1; Length 1029;	
Best Local Similarity	77.8%; Pred. No. 64;
Matches	7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KIFGSLAFL 9
|||||
Db 826 KIFGSLEIL 834

Search completed: November 14, 2000, 11:56:11
Job time: 89 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 14, 2000, 11:54:42 ; Search time 18.18 Seconds
(without alignments)
46.225 Million cell updates/sec

Title: US-09-277-074-10
Perfect score: 43
Sequence: 1 KIFGSLAFL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 297973 seqs, 93374136 residues

Total number of hits satisfying chosen parameters: 297973

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_14:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	100.0	1259	6	O18735
2	36	83.7	356	5	O44592
3	36	83.7	502	1	O74002
4	33	76.7	120	5	O20695
5	33	76.7	1760	5	O9VLT3
6	32	74.4	157	11	O63595
7	32	74.4	221	11	O9X230
8	32	74.4	223	11	O9Z1V5
9	32	74.4	231	5	O19158
10	32	74.4	454	5	O9XTU7
11	32	74.4	500	5	O9VKC2
12	31	72.1	50	10	O43282
13	31	72.1	149	12	O9YVW5
14	31	72.1	232	1	O26659
15	31	72.1	264	2	O9Z980
16	31	72.1	326	2	O9X0U7
17	31	72.1	335	5	O17809
18	31	72.1	343	5	O9UAX3
19	31	72.1	350	5	P91506

20	31	72.1	475	10	O23402
21	31	72.1	505	5	O9U2K5
22	31	72.1	552	5	O9V812
23	31	72.1	589	5	O9W1V0
24	31	72.1	616	10	O9SIX8
25	31	72.1	687	11	O9WU87
26	31	72.1	689	13	O9W701
27	31	72.1	962	5	O9TVU8
28	31	72.1	965	5	O44405
29	31	72.1	1142	5	O22528
30	31	72.1	3848	5	O76737
31	31	72.1	4199	2	P74440
32	30.5	70.9	2307	5	O9V496
33	30.5	70.9	3351	5	O94907
34	30	69.8	51	8	O20187
35	30	69.8	77	2	O9X1D7
36	30	69.8	80	2	O50893
37	30	69.8	99	2	P74900
38	30	69.8	161	3	O07990
39	30	69.8	184	11	P97453
40	30	69.8	184	11	P97297
41	30	69.8	222	2	P73366
42	30	69.8	287	8	O34935
43	30	69.8	288	8	O35993
44	30	69.8	336	5	O44697
45	30	69.8	338	5	O45710

ALIGNMENTS

RESULT 1

O18735
ID O18735 PRELIMINARY; PRT; 1259 AA.
AC O18735;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE ERBB-2.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
RN [1]
RP SEQUENCE FROM N.A.
RA Yokota H.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB008451; BAA23127.1; -
DR HSP; P00523; 2PTK.
DR INTERPRO; IPR000494; -
DR INTERPRO; IPR000719; -
DR INTERPRO; IPR001245; -
DR INTERPRO; IPR002048; -
DR INTERPRO; IPR002174; -
DR PFAM; PF00069; pkinase; 1.
DR PFAM; PF00757; Furin-like; 1.
DR PFAM; PF01030; Recep_L_domain; 2.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
SQ SEQUENCE 1259 AA; 137989 MW; E37364D49C4ACD46 CRC64;

Query Match 100.0%; Score 43; DB 6; Length 1259;

Best Local Similarity 100.0%; Pred. No. 2.5; 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIFGSLAFL 9

Db 369 KIFGSLAFL 377

RESULT 2

O44592 ID O44592 PRELIMINARY; PRT; 356 AA.
 AC O44592;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE F48G7.1 PROTEIN.
 GN F48G7.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX MEDLINE: 94150718.
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Lalster N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
 RA Smaldon N., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.,
 RA "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans.";
 RN Nature 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Clarke K., Wohlmann P., Harrison M.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF039044; AAC47951.1;
 DR INTERPRO: IPR00168;
 DR INTERPRO: IPR003002;
 DR PFAM: PF01461; 7tm_4; 1.
 SQ SEQUENCE 356 AA; 41323 MW; DEF906750193F6A4 CRC64;

Query Match 83.7%; Score 36; DB 5; Length 356;
 Best Local Similarity 66.7%; Pred. No. 18;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIFGSLAFL 9
 I:|||||:
 Db 13 KLFGALAFI 21

RESULT 3
 O74002 ID O74002 PRELIMINARY; PRT; 502 AA.
 AC O74002;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE HYPOTHETICAL 58.2 KDA PROTEIN PH1141.
 GN PH1141.
 OS Pyrococcus horikoshii.
 OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OT3;
 RX MEDLINE: 98344137.
 RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
 RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
 RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
 RA Funahashi T., Tanaka T., Kudo H., Yamazaki J., Kushida N., Oguchi A.,
 RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
 RA Masuchi Y., Shizuya H., Kikuchi H.;
 RT "Complete sequence and gene organization of the genome of a hyper-
 thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
 RL DNA Res. 5:55-76(1998).

DR EMBL: AF000005; BAA30241.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 502 AA; 58165 MW; 7228A9778B2707B1 CRC64;

Query Match 83.7%; Score 36; DB 1; Length 502;
 Best Local Similarity 87.5%; Pred. No. 25;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IFGSLAFL 9
 :|||||||
 Db 123 LFGSLAFL 130

RESULT 4
 Q20695 ID Q20695 PRELIMINARY; PRT; 120 AA.
 AC Q20695;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE COSMID F53B1.
 GN F53B1.3.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX MEDLINE: 94150718.
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Lalster N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
 RA Smaldon N., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.,
 RA "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans.";
 RN Nature 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Miller N.;
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Waterston R.;
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Waterston R.;
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U40953; AAB52646.1; -.
 SQ SEQUENCE 120 AA; 14016 MW; B7044AC89DCF2AF8 CRC64;

Query Match 76.7%; Score 33; DB 5; Length 120;
 Best Local Similarity 87.5%; Pred. No. 24;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 IFGSLAFL 9
 :|||||
 Db 98 IFGSLAFL 105

RESULT 5
 Q9VLT3

Qy 2 IFGSLAFL 9
: || || || |

Query Match 74.4%; Score 32; DB 11; Length 221;
Best Local Similarity 85.7%; Pred. NO. 70;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 FGSLAF 9
|||||
Db 189 FGSLAF 195

RESULT 8
Q921V5 ID Q921V5 PRELIMINARY; PRT; 223 AA.
AC Q921V5;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE OLFACTORY RECEPTOR B3 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BL/6; TISSUE=OLFACTORY EPITHELIUM;
RX MEDLINE: 99091050.
RA Krautwurst D., Yau K.W., Reed R.R.;
RT Identification of ligands for olfactory receptors by functional
expression of a receptor library.*;
RL Cell 95:917-926(1998).
DR EMBL: AF102518; AD13310.1; -.
DR INTERPRO: IPR000276; -.
DR INTERPRO: IPR000725; -.
DR PFAM: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODOPS.
DR PRINTS: PR00245; OLFACTORYR.
DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
FT NON_TER 1
FT NON_TER 223 223
SQ SEQUENCE 223 AA; 25089 MW; 83097D299076AF5E CRC64;

Query Match 74.4%; Score 32; DB 11; Length 223;
Best Local Similarity 85.7%; Pred. No. 70;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 FGSLAF 9
|||||
Db 189 FGSLAF 195

RESULT 9
Q19158 ID Q19158 PRELIMINARY; PRT; 231 AA.
AC Q19158;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-JAN-1999 (TREMBlrel. 09, Last annotation update)
DE F07C6.3 PROTEIN.
GN F07C6.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
OC Rhabditidae; Peloderinae; Caenorhabditis.
RN [1]
RP SEQUENCE FROM N.A.
RC Steward C.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 94150718.
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Shownkeen R.,
RA Smaildon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
RL Nature 368:32-38(1994).
DR EMBL: Z98866; CAB11549.1; -.
DR INTERPRO: IPR001617; -.
DR PFAM: PF00005; ABC_tran; 1.
SQ SEQUENCE 454 AA; 50540 MW; 222C49339347A70C CRC64;

RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Shownkeen R.,
RA Smaildon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
RL Nature 368:32-38(1994).
DR EMBL: Z69659; CAA93484.1; -.
SQ SEQUENCE 231 AA; 26252 MW; 1E8271FBE9111A58 CRC64;

Query Match 74.4%; Score 32; DB 5; Length 231;
Best Local Similarity 62.5%; Pred. No. 73;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIFGSLAF 8
:::|||||
Db 44 QVFGSI AF 51

RESULT 10
Q9XTU7 ID Q9XTU7 PRELIMINARY; PRT; 454 AA.
AC Q9XTU7;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE Y49E10.9 PROTEIN.
GN Y49E10.9.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
OC Rhabditidae; Peloderinae; Caenorhabditis.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 94150718.
RA Barlow K.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 94150718.
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Shownkeen R.,
RA Smaildon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
RL Nature 368:32-38(1994).
DR EMBL: Z98866; CAB11549.1; -.
DR INTERPRO: IPR001617; -.
DR PFAM: PF00005; ABC_tran; 1.
SQ SEQUENCE 454 AA; 50540 MW; 222C49339347A70C CRC64;

Query Match 74.4%; Score 32; DB 5; Length 454;
Best Local Similarity 66.7%; Pred. No. 14e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KIFGSLAF 9
:|:|:|:|
Db 439 KLFGLLAFV 447

RESULT 11
Q9VKC2 ID Q9VKC2 PRELIMINARY; PRT; 500 AA.

AC Q9VKC2; 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE CG12317 PROTEIN.
 DE CG12317
 GN Drosophila melanogaster (Fruit fly).
 OS Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY.
 RX MEDLINE; 20196006.
 RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foaier C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 DR EMBL; AE003634; ANF53154.1; -
 DR FLYBASE; FBgn0032403; CG12317.
 DR INTERPRO; IPR002027; -
 DR INTERPRO; IPR002293; -
 DR PFAM; PF00324; aa_permeases; 1.
 SQ SEQUENCE 500 AA; 54820 MW; 48BB44291114FEB8 CRC64;

Query Match 74.4%; Score 32; DB 5; Length 500;
 Best Local Similarity 55.6%; Pred. No. 1.6e+02;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KIFGSLAFL 9
 : : : : :
 Db 306 RVFGPLAFM 314

RESULT 12
 Q43282
 ID Q43282 PRELIMINARY; PRT; 50 AA.
 AC Q43282;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
 DE DISULFIDE-ISOMERASE (EC 5.3.4.1) (PROTEIN DISULFIDE ISOMERASE) (S-S
 DE REARRANGASE) (FRAGMENT).
 GN Arabidopsis thaliana (Mouse-ear cress).
 OS Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; Rosidae; eurosids II; Brassicales;
 OC Brassicaceae; Arabidopsids.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-FLOWER BUDS OF A THALIANA ECOTYPE COLUMBIA C24;
 RA Mache R., Quigley F., Thomas F., Yu D.;
 RL Submitted (NOV-1992) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: REARRANGEMENT OF BOTH INTRACHAIN AND
 CC INTERCHAIN DISULFIDE BONDS IN PROTEINS TO FORM THE NATIVE
 CC STRUCTURES.
 DR EMBL; Z18459; CAA79190.1; -
 DR MENDEL; 13106; Arath;2306;13106.
 KW isomerase.
 FT NON_TER 1 50
 FT NON_TER 50 50
 SQ SEQUENCE 50 AA; 5390 MW; 25DB1455B42FC682 CRC64;

Query Match 72.1%; Score 31; DB 10; Length 50;
 Best Local Similarity 85.7%; Pred. No. 25;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 FGSLAFL 9
 : : : : :
 Db 7 FGSLAFL 13

RESULT 13
 Q9YVV5 PRELIMINARY; PRT; 149 AA.
 ID Q9YVV5
 AC Q9YVV5;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
 DE ORF MSV137 HYPOTHETICAL PROTEIN.
 GN MSV137.
 OS Melanoplus sanguinipes entomopoxvirus.
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;
 OC Entomopoxvirus B.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-TUCSON;
 RX MEDLINE; 99102612.
 RA Afonso C.L., Tulman E.R., Lu Z., Oma E., Kutish G.F., Rock D.L.;
 RT "The genome of Melanoplus sanguinipes entomopoxvirus.";
 RL J. Virol. 73:533-552(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-TUCSON;
 RA Afonso C.L., Tulman E.R., Lu Z., Oma E., Kutish G.F., Rock D.L.;
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF063866; AAC97669.1; -
 SQ SEQUENCE 149 AA; 17849 MW; 867139E34BE87407 CRC64;

Query Match 72.1%; Score 31; DB 12; Length 149;
 Best Local Similarity 55.6%; Pred. No. 74;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KIFGSLAFL 9
 : : : : :
 Db 41 KIFGSLAFL 49

RESULT 14
 O26659

Search completed: November 14, 2000, 11:55:43
Job time: 61 sec

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ID O26659      PRELIMINARY;      PRT;      232 AA.
AC O26659;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE CONSERVED PROTEIN.
GN MTH559.
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
OC Methanobacterium.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DELTA H;
RX MEDLINE; 98037514.
RA Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., DuBois J.,
RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
RA Harrilson D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jiwni N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Nolling J., Reeve J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
RT deltaH: functional analysis and comparative genomics.";
RL J. Bacteriol. 179:7135-7155(1997).
DR EMBL; AE000838; AAB85065.1; -.
DR INTERPRO; IPR002829; -.
DR PFAM; PF01976; DUF116; 1.
DR PRODOM; PD013292; -. 1.
SQ SEQUENCE 232 AA; 26259 MW; BBF39317E95A58ED CRC64;

Query Match      72.1%; Score 31; DB 1; Length 232;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KIFGSLAFL 9
   :||| | |
DB 9 QIEGQLVFL 17

RESULT 15
Q9Z980
ID Q9Z980      PRELIMINARY;      PRT;      264 AA.
AC Q9Z980;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE YBBP FAMILY HYPOTHETICAL PROTEIN.
GN YBBP.
OS Chlamydia pneumoniae (Chlamydia pneumoniae).
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CWL029;
RX MEDLINE; 99206606.
RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
RL Nat. Genet. 21:385-389(1999).
DR EMBL; AE001596; AAD18254.1; -.
SQ SEQUENCE 264 AA; 30237 MW; 755874E5FD16EDF8 CRC64;

Query Match      72.1%; Score 31; DB 2; Length 264;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 IFGSLAFL 9
   :|| | | |
DB 38 VFGLAFL 45

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 14, 2000, 11:56:53 ; Search time 8.45 Seconds
(without alignments)
34.027 Million cell updates/sec

Title: US-09-277-074-10
Perfect score: 43
Sequence: 1 KIFGSLAFL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 87993 seqs, 31947931 residues

Total number of hits satisfying chosen parameters: 1088

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	51.2	19	1	DURB_STRGW
2	21	48.8	7	1	UN06_PINPS
3	19	44.2	13	1	CRBL_VESTR
4	19	44.2	13	1	UP51_UPEIN
5	19	44.2	14	1	GR75_CANFA
6	19	44.2	18	1	PHTP_PSESE
7	18	41.9	19	1	DURA_STRGV
8	17	39.5	12	1	NUDM_CANFA
9	17	39.5	13	1	CRBL_VESAN
10	17	39.5	13	1	CRBL_VESXA
11	17	39.5	15	1	LMA2_LOCMI
12	17	39.5	16	1	UPAB_HUMAN
13	16	37.2	12	1	PSP3_PHYPA
14	16	37.2	13	1	PSP3_PINPS
15	16	37.2	14	1	UC18_MAIZE
16	16	37.2	16	1	PPAC_BACME
17	16	37.2	17	1	ATPI_PAVLU
18	16	37.2	18	1	AHD2_TETPY
19	16	37.2	18	1	NPA_BOVIN
20	16	37.2	18	1	SFAH_HELAN
21	16	37.2	19	1	HBB2_URORA
22	16	37.2	19	1	HHP_THICU
23	16	37.2	19	1	LANC_STRSQ
24	16	37.2	19	1	MDH_BREDI
25	16	37.2	19	1	MDH_BREVE
26	16	37.2	20	1	CATA_ACIRA
27	16	37.2	20	1	GR78_PHAVU
28	16	37.2	20	1	V101_VACCV
29	15	34.9	9	1	AL11_CARMA
30	15	34.9	9	1	NSK1_SARBU
31	15	34.9	10	1	LSK2_LEUMA
32	15	34.9	11	1	LSK1_LEUMA
33	15	34.9	11	1	LSKP_PERAM

34	15	34.9	11	1	TKC2_CALVO
35	15	34.9	12	1	LOSK_LOCMI
36	15	34.9	14	1	NSK2_SARBU
37	15	34.9	14	1	TEMC_RANTE
38	15	34.9	14	1	TEMC_RANTE
39	15	34.9	15	1	COXI_THUOB
40	15	34.9	15	1	FIBA_SYNCA
41	15	34.9	17	1	BOL3_MEGPE
42	15	34.9	17	1	BOL5_MEGPE
43	15	34.9	19	1	PTHP_STRSA
44	15	34.9	19	1	UP21_UPEIN
45	15	34.9	19	1	UP22_UPEIN

ALIGNMENTS

RESULT 1

DURB_STRGW STANDARD; PRT; 19 AA.
AC P36502;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE LANTIBIOTIC DURAMYCIN B.
OS Streptovorticillium sp. (strain R2075).
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae;
OC Streptovorticillium.
RN [1]
RP SEQUENCE.
RX MEDLINE; 91107436.
RA Fredenhagen A., Fendrich G., Markl F., Markl W., Gruner J.,
RA Raschdorf F., Peter H.H.;
RT "Duramycins B and C, two new lanthionine containing antibiotics as
RT inhibitors of phospholipase A2. Structural revision of duramycin and
RT cinnamycin.";
J. Antibiot. 43:1403-1412(1990).
RN [2]
RP STRUCTURE BY NMR.
RA Zimmermann N., Freund S., Fredenhagen A., Jung G.;
RT "Solution structure of the lantibiotics duramycin B and C.";
RL (in) Schneider C.H., Eberles A.N. (eds.);
RL Peptides 1992, pp.519-520, Escrom Science Publishers, Leiden (1993).
RN [3]
RP STRUCTURE BY NMR.
RX MEDLINE; 93387292.
RA Zimmermann N., Freund S., Fredenhagen A., Jung G.;
RT "Solution structures of the lantibiotics duramycin B and C.";
RL Eur. J. Biochem. 216:419-428(1993).
CC -1- FUNCTION: ACTS AS INHIBITOR OF PHOSPHOLIPASE A2.
CC -1- PTM: MATURATION OF LANTIBIOTICS INVOLVES THE ENZYMIC CONVERSION OF
CC THR, SER, AND CYS INTO DEHYDRATED AA AND THE FORMATION OF SULFIDE
CC BRIDGES. THIS IS FOLLOWED BY THE MEMBRANE TRANSLATION AND
CC CLEAVAGE OF THE MODIFIED PRECURSOR.
CC -1- SIMILARITY: STRUCTURAL SIMILARITY TO OTHER TYPE B LANTIBIOTICS.
KW Antibiolic; Lantibiotic.
FT MOD_RES 4 4
FT MOD_RES 6 6
FT MOD_RES 11 11
FT MOD_RES 18 18
FT MOD_RES 19 19
FT THIOETH 1 18
FT THIOETH 4 14
FT THIOETH 5 11
SQ SEQUENCE 19 AA; 2063 MW; 0133445627362F00 CRC64;
D-ALANINE.
D-ALANINE (BONDED TO 19).
D-ABU (AMINO BUTYRIC ACID).
D-ABU (AMINO BUTYRIC ACID).
LYSINOALANINE (BONDED TO 6).
ABU-S-CYS (METHYLLANTHIONINE).
ALA-S-CYS (LANTHIONINE).
ABU-S-CYS (METHYLLANTHIONINE).

Query Match 51.2%; Score 22; DB 1; Length 19;
Best Local Similarity 57.1%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 3 FGSLAFL 9

Db 7 FCPLTFV 13

RESULT 2
UN06_PINPS STANDARD; PRT; 7 AA.
ID UN06_PINPS
AC P81675;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE UNKNOWN PROTEIN FROM 2D-PAGE OF NEEDLES (N141) (FRAGMENT).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Coniferopsida; Coniferales; Pinaceae; Pinus.
RN [1]
RP SEQUENCE.
RC TISSUE=NEEDLE;
RX MEDLINE; 99274088.
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins";
RL Electrophoresis 20:1098-1108(1999).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.6, ITS MW IS: 25 KDA.
FT NON_TER 1 1
FT NON_TER 7 7
SQ SEQUENCE 7 AA; 823 MW; 69D76724486B5740 CRC64;

Query Match 48.8%; Score 21; DB 1; Length 7;
Best Local Similarity 42.9%; Pred. No. 8.8e+04;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 IFGSLAF 8
Db 1 LYGNLPF 7

RESULT 3
CRBL_VESTR STANDARD; PRT; 13 AA.
ID CRBL_VESTR
AC P17231;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE VESPID CHEMOTACTIC PEPTIDE T (VESCP-T).
OS Vespa tropica (Hornet).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Aculeata;
OC Vespoidea; Vespidae; Vespinae; Vespa.
RN [1]
RP SEQUENCE.
RC TISSUE=VENOM;
RA Yasuhara T., Nakajima T., Erspaer V.;
RL (in) Sakakibara S. (eds.);
RL Peptide chemistry 1982, pp.213-218, Protein Research Foundation,
RL Osaka (1983).
CC -1- FUNCTION: MAST CELL DEGRANULATING PEPTIDE. INDUCES THE CHEMOTAXIS
CC OF NEUTROPHILS.
KW Mast cell degranulation; Chemotaxis; Venom; Amidation.
FT MOD_RES 13 13
SQ SEQUENCE 13 AA; 1354 MW; 220140365DFE5338 CRC64;

Query Match 44.2%; Score 19; DB 1; Length 13;
Best Local Similarity 66.7%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KIFGSL 6
Db 7 KILGGL 12

RESULT 4

UP51_UPEIN STANDARD; PRT; 13 AA.
ID UP51_UPEIN
AC P82036;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE UPERIN 5.1.
OS Uperoleia inundata (Floodplain toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC Uperoleia.
RN [1]
RP SEQUENCE AND MASS SPECTROMETRY.
RC TISSUE=SKIN SECRETION;
RA Bradford A.M., Raftery M.J., Bowie J.H., Tyler M.J., Wallace J.C.,
RA Adams G.W., Severini C.;
RT "Novel uperin peptides from the dorsal glands of the Australian
RT floodplain toadlet Uperoleia inundata";
RL Aust. J. Chem. 49:475-484(1996).
CC -1- FUNCTION: UNKNOWN.
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC -1- MASS SPECTROMETRY: MW=1426; METHOD=FAB.
KW Amphibian skin.
SQ SEQUENCE 13 AA; 1457 MW; 290CA148C384B5A7 CRC64;

Query Match 44.2%; Score 19; DB 1; Length 13;
Best Local Similarity 75.0%; Pred. No. 4.7e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IFGS 5
Db 10 VFCS 13

RESULT 5
GR75_CANFA STANDARD; PRT; 14 AA.
ID GR75_CANFA
AC P99502;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE MITOCHONDRIAL STRESS-70 PROTEIN (75 KDA GLUCOSE REGULATED PROTEIN)
DE (GRP 75) (FRAGMENT).
OS HSPA9.
GN Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Carnivora; Canidae; Canis.
RN [1]
RP SEQUENCE.
RC TISSUE=HEART;
RX MEDLINE; 98163340.
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT dog heart proteins";
RL Electrophoresis 18:2795-2802(1997).
CC -1- FUNCTION: IMPLICATED IN THE CONTROL OF CELL PROLIFERATION AND
CC CELLULAR AGING. MAY ALSO ACT AS A CHAPERONE.
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL.
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
DR HSC-2DPAGE; P99502; DOG.
DR INTERPRO: IPR001023; -;
DR PROSITE; PS00297; HSP70_1; PARTIAL.
DR PROSITE; PS00329; HSP70_2; PARTIAL.
DR PROSITE; PS01036; HSP70_3; PARTIAL.
KW ATP-binding; Mitochondrion.
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1438 MW; 2AAEDD1AACBAC8D8 CRC64;

Query Match 44.2%; Score 19; DB 1; Length 14;
 Best Local Similarity 37.5%; Pred. No. 5.1e+02;
 Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 2 IFGSLAFL 9
 Db 5 IFGAVXI 12

RESULT 6
 PHPT_PSESE STANDARD; PRT; 18 AA.
 AC P25271; 1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 01-MAY-1992 (Rel. 22, Last annotation update)
 DE PHEROMONOTROPIN (PSS-PT).
 OS Pseudaletia separata (Armyworm).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Noctuoidea; Noctuidae; Hadeninae; Pseudaletia.
 RN [1]
 RP SEQUENCE.
 RC TISSUE-HEAD;
 RX MEDLINE; 92134266.
 RA Matsumoto S., Fonagy A., Kurihara M., Uchiumi K., Nagamine T.,
 RA Chijimatsu M., Mitsui T.;
 RT "Isolation and primary structure of a novel pheromonotropic
 RT neuropeptide structurally related to leucopyrokinin from the armyworm
 RT larvae, Pseudaletia separata.";
 RL Biochem. Biophys. Res. Commun. 182:534-539(1992).
 CC -1- FUNCTION: HORMONE THAT CONTROLS SEX PHEROMONE PRODUCTION IN
 CC LARVAE.
 CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
 CC PIR: JS0647; JS0647.
 DR INTERPRO: IPR001484;
 DR PROSITE: PS00539; PYROKININ; 1.
 FW Hormone; Neuropeptide; Amidation; Pyrokinin.
 FT MOD_RES 18
 FT AMIDATION.
 SQ SEQUENCE 18 AA; 2200 MW; DDF3A1B75ACB18FF CRC64;

Query Match 44.2%; Score 19; DB 1; Length 18;
 Best Local Similarity 37.5%; Pred. No. 6.5e+02;
 Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 1 KIFGSLAF 8
 Db 7 KVFENVEF 14

RESULT 7
 DURA_STRGV STANDARD; PRT; 19 AA.
 AC P36504;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE LANTIBIOTIC DURAMYCIN (LEUCOPEPTIN) (ANTIBIOTIC PA48009).
 OS Streptovorticillum griseovorticillatum.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae;
 OC Streptovorticillum.
 RN [1]
 RP SEQUENCE, AND STRUCTURE BY NMR.
 RC STRAIN=PA-48009;
 RX MEDLINE; 91107438.
 RA Hayashi F., Nagashima K., Terui Y., Kawamura Y., Matsumoto K.,
 RA Itazaki H.;
 RT "The structure of PA48009: the revised structure of duramycin.";
 RL J. Antibiot. 43:1421-1430(1990).
 RN [2]
 RP SEQUENCE.

RX MEDLINE; 91107436.
 RA Fredenhagen A., Fendrich G., Markl F., Markl W., Gruner J.,
 RA Raschdorf F., Peter H.H.;
 RT "Duramycins B and C, two new lanthionine containing antibiotics as
 RT inhibitors of phospholipase A2. Structural revision of duramycin and
 RT cinnamycin.";
 RL J. Antibiot. 43:1403-1412(1990).
 CC -1- FUNCTION: ACTS AS INHIBITOR OF PHOSPHOLIPASE A2.
 CC -1- PTM: MATURATION OF LANTHIBIOTICS INVOLVES THE ENZYMIC CONVERSION OF
 CC THR, SER, AND CYS INTO DEHYDRATED AA AND THE FORMATION OF SULFIDE
 CC BRIDGES. THIS IS FOLLOWED BY THE MEMBRANE TRANSLOCATION AND
 CC CLEAVAGE OF THE MODIFIED PRECURSOR
 CC -1- SIMILARITY: STRUCTURAL SIMILARITY TO OTHER TYPE B LANTHIBIOTICS.
 KW Antibiotic; Lanthibiotic.
 FT MOD_RES 4 4
 FT MOD_RES 6 6
 FT MOD_RES 11 11
 FT MOD_RES 18 18
 FT MOD_RES 19 19
 FT MOD_RES 19 19
 FT THIOETH 1 18
 FT THIOETH 4 14
 FT THIOETH 5 11
 SQ SEQUENCE 19 AA; 2069 MW; 012951AE27362F00 CRC64;

Query Match 41.9%; Score 18; DB 1; Length 19;
 Best Local Similarity 42.9%; Pred. No. 1.1e+03;
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 3 FGSLAFL 9
 Db 7 FGPTFV 13

RESULT 8
 NUDM_CANFA STANDARD; PRT; 12 AA.
 ID NUDM_CANFA
 AC P54713;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE NADH-UBIQUINONE OXIDOREDUCTASE 42 KDA SUBUNIT (EC 1.6.5.3)
 DE (EC 1.6.99.3) (COMPLEX I-42KD) (CI-42KD) (FRAGMENT).
 GN NDUF410.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 RN [1]
 RP SEQUENCE.
 RC TISSUE=HEART;
 RX MEDLINE; 98163340.
 RA Dunn M.J., Corbett J.M., Wheeler C.H.;
 RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
 RT dog heart proteins.";
 RL Electrophoresis 18:2795-2802(1997).
 CC -1- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY
 CC CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED
 CC TO BE UBIQUINONE.
 CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
 CC -1- COFACTOR: FAD; CONTAINS ONE NONCOVALENTLY BOUND FAD PER
 CC POLYPEPTIDE CHAIN.
 CC -1- SUBUNIT: COMPLEX I IS COMPOSED OF ABOUT 40 DIFFERENT SUBUNITS.
 CC THIS A COMPONENT OF THE HYDROPHOBIC PROTEIN FRACTION.
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
 CC HSC-2DPAGE; P54713; DOG.
 KW Oxidoreductase; NAD; Ubiquinone; Flavoprotein; FAD; Mitochondrion.
 FT NON_TER 12
 FT 12
 SQ SEQUENCE 12 AA; 1284 MW; 3CCD4E2B36EDD737 CRC64;

Query Match 39.5%; Score 17; DB 1; Length 12;
 Best Local Similarity 42.9%; Pred. No. 1.1e+03;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 FGSLAF 9
: | | |
Db 3 YGPLAXI 9

RESULT 9
CRBL_VESAN STANDARD; PRT; 13 AA.
AC P17233;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 13-DEC-1998 (Rel. 37, Last annotation update)
DE VESPID CHEMOTACTIC PEPTIDE A (VESP-C-A).
OS Vespa analis (Hornet).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Vespoidae; Vespidae; Vespinae; Vespa.
[1]
RP SEQUENCE.
RC TISSUE=VENOM;
RA Yasuhara T., Nakajima T., Fukuda K., Tsukamoto Y., Mori M., Kitada C.,
RA Fujino M.;
RL (In) Muekata E. (eds.);
RL Peptide Chemistry 1983, pp.185-190, Protein Research Foundation,
RL Osaka (1984).
CC -1- FUNCTION: MAST CELL DEGRANULATING PEPTIDE. INDUCES THE CHEMOTAXIS
CC OF NEUTROPHILS.
KW Mast cell degranulation; Chemotaxis; Venom; Amidation.
FT MOD_RES 13
SQ SEQUENCE 13 AA; 1386 MW; C85554365DF9233D CRC64;

Query Match 39.5%; Score 17; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KIFGSL 6
: | | |
Db 7 KLLGGL 12

RESULT 10
CRBL_VESXA STANDARD; PRT; 13 AA.
AC P17234;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 13-DEC-1998 (Rel. 37, Last annotation update)
DE VESPID CHEMOTACTIC PEPTIDE X (VESP-C-X).
OS Vespa xanthoptera (Japanese hornet).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Vespoidae; Vespidae; Vespinae; Vespa.
[1]
RP SEQUENCE.
RC TISSUE=VENOM;
RA Yasuhara T., Itokawa H., Suzuki N., Nakamura H., Nakajima T.;
RL (In) Izumiya N. (eds.);
RL Peptide Chemistry 1984, pp.177-182, Protein Research Foundation,
RL Osaka (1985).
CC -1- FUNCTION: MAST CELL DEGRANULATING PEPTIDE. INDUCES THE CHEMOTAXIS
CC OF NEUTROPHILS.
KW Mast cell degranulation; Chemotaxis; Venom; Amidation.
FT MOD_RES 13
SQ SEQUENCE 13 AA; 1368 MW; C85040365DF9233D CRC64;

Query Match 39.5%; Score 17; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KIFGSL 6

Db 7 KLLGGL 12

RESULT 11
LMA2_LOCMI STANDARD; PRT; 15 AA.
AC P38497;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE LOM-AG-MYOTROPIN II (ACCESSORY GLAND MYOTROPIN II).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
OC Acridomorpha; Acridoidea; Acrididae; Locusta.
[1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=MALE ACCESSORY GLAND;
RA Paemen L., Schoofs L., Proost P., Decock B., de Loof A.;
RT Isolation, identification and synthesis of Lom-AG-myotropin II, a
RT novel peptide in the male accessory reproductive glands of Locusta
RT migratoria.*;
RL Insect Biochem. 21:243-248(1991).
CC -1- FUNCTION: MYOTROPIC PEPTIDE.
CC -1- TISSUE SPECIFICITY: MALE ACCESSORY GLANDS.
KW Neuropeptide.
SQ SEQUENCE 15 AA; 1592 MW; 8C80FFF4B41941CF CRC64;

Query Match 39.5%; Score 17; DB 1; Length 15;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 FGSL 6
: | | |
Db 9 FGAL 12

RESULT 12
UPAB_HUMAN STANDARD; PRT; 16 AA.
AC P31935;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE UNKNOWN PROTEIN FROM 2D-PAGE OF PLASMA (SPOT 53) (FRAGMENTS).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
[1]
RP SEQUENCE.
RC TISSUE=PLASMA;
RX MEDLINE; 94147970.
RA Pasquali C., Sanchez J.-C., Tissot J.-D., Appel R.D., Walzer C.,
RA Balant L., Hochstrasser D.F.;
RT Plasma and red blood cell protein maps: update 1993.*;
RL Electrophoresis 14:1223-1231(1993).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.9, ITS MW IS: 41 KDA.
DR SWISS-2DPAGE; P31935; HUMAN.
FT NON_TER 1
FT NON_CONS 7
FT NON_TER 16
FT NON_CONS 16
SQ SEQUENCE 16 AA; 1879 MW; D63C5047818114B2 CRC64;

Query Match 39.5%; Score 17; DB 1; Length 16;
Best Local Similarity 57.1%; Pred. No. 1.5e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 FGSLAF 9

```
Db 4 FLXLAYL 10
RESULT 13
PSP3_PHYPA
ID PSP3_PHYPA STANDARD: PRT: 12 AA.
AC P80662;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE OXYGEN-EVOLVING ENHANCER PROTEIN 2 (OEE2) (24 KDA SUBUNIT OF OXYGEN
DE EVOLVING SYSTEM OF PHOTOSYSTEM II) (FRAGMENT).
OS Physcomitrella patens (Moss).
OC Eukaryota; Viridiplantae; Embryophyta; Bryophyta; Bryopsida;
OC Funariidae; Funariales; Funariaceae; Physcomitrella.
RN [1]
RP SEQUENCE.
RC TISSUE=PROTONEMA;
RX MEDLINE: 97275459.
RA Kasten B., Buck F., Nuske J., Reski R.;
RT "Cytokinin affects nuclear- and plastome-encoded energy-converting
RT plastid enzymes.";
RL Planta 201:261-272(1997).
CC -1- FUNCTION: ASSOCIATED WITH THE OXYGEN-EVOLVING COMPLEX OF
CC PHOTOSYSTEM II.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE; ASSOCIATED
CC WITH THE PHOTOSYSTEM II COMPLEX.
CC -1- INDUCTION: BY LIGHT.
CC -1- SIMILARITY: TO OTHER OEE2 SUBUNITS.
KW Photosynthesis; Photosystem II; Chloroplast; Thylakoid membrane;
KW Multigene family.
FT NON_TER 12
SQ SEQUENCE 12 AA: 1182 MW; 8D2B0D54D7C44DC5 CRC64;

Query Match 37.2%; Score 16; DB 1; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.8e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IFGS 5
Db 8 VFGA 11

RESULT 14
PSBP_PINPS
ID PSBP_PINPS STANDARD: PRT: 13 AA.
AC P81668;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE OXYGEN-EVOLVING ENHANCER PROTEIN 2 (OEE2) (23 KDA SUBUNIT OF OXYGEN
DE EVOLVING SYSTEM OF PHOTOSYSTEM II) (FRAGMENT).
GN PSBP.
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Coniferopsida; Coniferales; Pinaceae; Pinus.
RN [1]
RP SEQUENCE.
RC TISSUE=NEEDLE;
RX MEDLINE: 99274088.
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins.";
RL Electrophoresis 20:1098-1108(1999).
CC -1- FUNCTION: ASSOCIATED WITH THE OXYGEN-EVOLVING COMPLEX OF
CC PHOTOSYSTEM II (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE; ASSOCIATED
CC WITH THE PHOTOSYSTEM II COMPLEX (BY SIMILARITY).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN
CC (SPOT N179) IS: 5.9, ITS MW IS: 22 KDA.

CC -1- SIMILARITY: TO OTHER OEE2 SUBUNITS.
KW Photosynthesis; Photosystem II; Chloroplast; Thylakoid membrane.
FT NON_TER 13
SQ SEQUENCE 13 AA: 1294 MW; C6772B0D54D7C44D CRC64;

Query Match 37.2%; Score 16; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 2e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IFGS 5
Db 8 VFGA 11

RESULT 15
UC18_MAIZE
ID UC18_MAIZE STANDARD: PRT: 14 AA.
AC P80624;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE UNKNOWN PROTEIN FROM 2D-PAGE OF ETIOLATED COLEOPTILE (SPOT 263)
DE (FRAGMENT).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
RN [1]
RP SEQUENCE.
RC TISSUE=COLEOPTILE;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.1, ITS MW IS: 50.3 KDA.
DR MAIZE-2DPAGE; P80624; COLEOPTILE.
DR MAIZE2DB; 123950; -.
FT NON_TER 14
SQ SEQUENCE 14 AA: 1485 MW; 2EF9116472A39458 CRC64;

Query Match 37.2%; Score 16; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IFG 4
Db 8 IFG 10

RESULT 16
PPAC_BACME
ID PPAC_BACME STANDARD: PRT: 16 AA.
AC P56948;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE MANGANESE-DEPENDENT INORGANIC PYROPHOSPHATASE (EC 3.6.1.1)
DE (PYROPHOSPHATE PHOSPHO-HYDROLASE) (PPASE) (FRAGMENT).
GN PPAC.
OS Bacillus megaterium.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
RN [1]
RP SEQUENCE.
RX MEDLINE: 98455825.
RA Young T.W., Kuhn N.J., Wadeson A., Ward S., Burges D., Cooke G.D.;
RT "Bacillus subtilis ORF yyoQ encodes a manganese-dependent inorganic
RT pyrophosphatase with distinctive properties: the first of a new class
RT of soluble pyrophosphatase?";
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RL Microbiology 144:2563-2571(1998).
CC -1- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O -> 2 ORTHOPHOSPHATE.
CC -1- COFACTOR: REQUIRES MANGANESE FOR ITS ACTIVITY.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE PPASE CLASS C FAMILY.
KW Hydrolase; Manganese.
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1828 MW; 3C0E6735D98B38A0 CRC64;

Query Match 37.2%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IFG 4
DB 5 IFG 7

RESULT 17
ID ATPI_PAVLU STANDARD; PRT; 17 AA.
AC P28529;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ATP SYNTHASE A CHAIN (EC 3.6.1.34) (SUBUNIT IV) (FRAGMENT).
GN ATPI.
OS Pavlova lutheri (Monochrysis lutheri).
OC Chloroplast.
CC Eukaryota; Haptophyceae; Pavlovales; Pavlova.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 92316212.
RA Scaramuzzi C.D., Stokes H.W., Hiller R.G.;
RT "Characterisation of a chloroplast-encoded secy homologue and atph from a chromophytic alga. Evidence for a novel chloroplast genome organisation";
RL FEBS Lett. 304:119-123(1992).
CC -1- FUNCTION: KEY COMPONENT OF THE PROTON CHANNEL; IT MAY PLAY A DIRECT ROLE IN THE TRANSLLOCATION OF PROTONS ACROSS THE MEMBRANE.
CC -1- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0) HAS THREE MAIN SUBUNITS: A, B AND C.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. CHLOROPLAST THYLAKOID MEMBRANE.
CC -1- SIMILARITY: BELONGS TO THE ATPASE A CHAIN FAMILY.

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CC EMBL: X64731; CAA45996.1; -
DR PIR: S23423; S23423.
DR MENDEL: 2272; PAVlu;atpi;1.
DR INTERPRO: IPR000568; -
DR PROSITE: PS00449; ATPASE_A; PARTIAL.
KW Hydrogen ion transport; CF(0); Chloroplast; Transmembrane.
FT NON_TER 1 1
FT TRANSMEM <1 13 POTENTIAL.
SQ SEQUENCE 17 AA; 1753 MW; F313DCE74C23CF2E CRC64;

Query Match 37.2%; Score 16; DB 1; Length 17;
Best Local Similarity 50.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 IFGLA 7

DB 3 IFATLS 8
RESULT 18
ID AHD2_TETPY STANDARD; PRT; 18 AA.
AC P35430;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE 20-ALPHA-HYDROXYSTEROID DEHYDROGENASE (EC 1.1.1.149) (20-ALPHA-HSD) (FRAGMENT).
OS Tetrahymena pyriformis.
CC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymena.
RN [1]
RP SEQUENCE, AND CHARACTERIZATION.
RX STRAIN=W;
RX MEDLINE: 94107273.
RA Inazu A., Sato K., Nakayama Y., Hara A., Nozawa Y.;
RT "Purification and characterization of a novel dimeric 20 alpha-hydroxysteroid dehydrogenase from Tetrahymena pyriformis";
RL Biochem. J. 297:195-200(1994).
CC -1- FUNCTION: SPECIFIC FOR THE OXIDATION OF THE 20-ALPHA-HYDROXY GROUP OF 17-ALPHA-HYDROXYPROGESTERONE AND 17-ALPHA-HYDROXYPROGESTERONE.
CC -1- CATALYTIC ACTIVITY: 17-ALPHA, 20-ALPHA-DIHYDROXYPREGN-4-EN-3-ONE + NAD(P)(+) -> 17-ALPHA-HYDROXYPROGESTERONE + NAD(P)H.
CC -1- SUBUNIT: HOMODIMER.
DR PIR: S40502; S40502.
KW Oxidoreductase; NADP.
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 1861 MW; 16DF6B287E3B0A0D CRC64;

Query Match 37.2%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IFG 4
DB 15 IFG 17

RESULT 19
ID NPA_BOVIN STANDARD; PRT; 18 AA.
AC P15506;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-APR-1990 (Rel. 14, Last annotation update)
DE NEUROPEPTIDE A.
OS Bos taurus (Bovine).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
RN [1]
RP SEQUENCE.
RX TISSUE=BRAIN;
RX MEDLINE: 86067985.
RA Yang H.-Y.T., Fratta W., Majane E.A., Costa E.;
RT "Isolation, sequencing, synthesis, and pharmacological characterization of two brain neuropeptides that modulate the action of morphine";
RL Proc. Natl. Acad. Sci. U.S.A. 82:7757-7761(1985).
CC -1- FUNCTION: MODULATES THE ACTION OF MORPHINE.
DR PIR: A24749; A24749.
KW Neuropeptide; Amidation.
FT SIMILAR 15 18 TO NEUROPEPTIDE B (AA 5-8) (IDENTICAL).
FT MCD_RES 18 18 AMIDATION.
SQ SEQUENCE 18 AA; 1921 MW; EC52DAE1F45CFCFB CRC64;

Query Match 37.2%; Score 16; DB 1; Length 18;
 Best Local Similarity 80.0%; Pred. No. 2.7e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 FGSIA 7
 DB 9 FWSIA 13

RESULT 20

SFAH_HELAN STANDARD; PRT; 18 AA.
 ID SFAH_HELAN
 AC P81098;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE SPED FATNY ACYL-ESTER HYDROLASE (EC 3.1.1.1) (FRAGMENT).
 OS Helianthus annuus (Common sunflower).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae;
 OC euasterids II; Asterales; Asteraceae; Asterioideae; Heliantheae;
 OC Helianthus.
 RN [1]
 RP SEQUENCE.
 RC STRAIN=CV. RUSTICA / VAR. EUROFLOR; TISSUE=SEED;
 RA Beisson F., Gardies A.-M., Teissere M., Ferte N., Noat G.;
 RT "An esterase neosynthesized in post-germinated sunflower seeds is
 related to a new family of lipolytic enzymes.";
 RL Plant Physiol. Biochem. 35:761-765(1997).
 [2]
 RN CHARACTERIZATION.
 RP MEDLINE; 95210327.
 RA Teissere M., Borel M., Caillol B., Nari J., Gardies A.-M., Noat G.;
 RT "Purification and characterization of a fatty acyl-ester hydrolase
 from post-germinated sunflower seeds.";
 RL Biochim. Biophys. Acta 1255:105-112(1995).
 CC -1- FUNCTION: IMPLICATED IN THE BREAKDOWN OF OIL BODY-STORED LIPIDS
 DURING POST-GERMINATION.
 CC -1- CATALYTIC ACTIVITY: A CARBOXYLIC ESTER + H(2)O = AN ALCOHOL + A
 CARBOXYLIC ANION.
 CC -1- TISSUE SPECIFICITY: SEED.
 CC -1- DEVELOPMENTAL STAGE: POST-GERMINATION.
 CC -1- SIMILARITY: BELONGS TO THE "GDSL" FAMILY OF LIPOLYTIC ENZYMES.
 DR INTERPRO: IPR001087; .
 DR PROSITE: PS01098; LIPASE_GDSL_SER; PARTIAL.
 KW Hydrolase; Lipid degradation; Glycoprotein.
 FT ACT_SITE 13 13 BY SIMILARITY.
 FT NON_TER 18 18
 SQ SEQUENCE 18 AA; 2057 MW; 3E9A80BB6548E862 CRC64;

Query Match 37.2%; Score 16; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IFG 4
 DB 9 IFG 11

RESULT 21

IBB2_UROHA STANDARD; PRT; 19 AA.
 ID IBB2_UROHA
 AC P18992;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-NOV-1991 (Rel. 18, Last annotation update)
 DE HEMOGLOBIN BETA-2 CHAIN (FRAGMENT).
 OS Uromastix hardwickii (Indian spiny-tailed lizard).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Leiolepineae;
 OC Uromastix.

[1]
 RN SEQUENCE.
 RP MEDLINE; 84029159.
 RA Naqvi S., Zaidi Z.H., von Bahr-Lindstroem H., Carlquist M.,
 RA Joernvall H.;
 RT "Characterization of hemoglobin from the lizard Uromastix
 hardwickii.";
 RL FEBS Lett. 162:290-295(1983).
 DR PIR; A05305; A05305.
 DR INTERPRO: IPR000971; .
 DR PROSITE: PS01033; GLOBIN; PARTIAL.
 KW Heme; Oxygen transport; Respiratory protein; Erythrocyte.
 FT NON_TER 1 1
 FT NON_TER 19 19
 SQ SEQUENCE 19 AA; 1914 MW; C40AD8EA30019057 CRC64;

Query Match 37.2%; Score 16; DB 1; Length 19;
 Best Local Similarity 40.0%; Pred. No. 2.8e+03;
 Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 FGSIA 7
 DB 5 FGNIS 9

RESULT 22

HHP_THICU STANDARD; PRT; 19 AA.
 ID HHP_THICU
 AC P80487;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE HETEROTROPH-SPECIFIC PROTEIN (FRAGMENT).
 OS Thioabacillus cuprinus.
 OC Bacteria; Proteobacteria; beta subdivision; Comamonadaceae; Thiomonas.
 RN [1]
 RP SEQUENCE.
 RC STRAIN=DSM 5494;
 RA Marin I., Amaro A.M., Jerez C.A., Amils R., Abad J.P.;
 RL Submitted (SEP-1995) to the SWISS-PROT data bank.
 CC -1- MISCELLANEOUS: FOUND SPECIFICALLY IN CELLS CULTURED
 HETEROTROPHICALLY.
 CC NON_TER 19 19
 FT NON_TER 19 19
 SQ SEQUENCE 19 AA; 1786 MW; C549197D0A492B07 CRC64;

Query Match 37.2%; Score 16; DB 1; Length 19;
 Best Local Similarity 50.0%; Pred. No. 2.8e+03;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 IFGSIA 7
 DB 8 VIGSAA 13

RESULT 23

LANC_STRSQ STANDARD; PRT; 19 AA.
 ID LANC_STRSQ
 AC P38655;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE LANTIBIOTIC ANCOVENIN.
 OS Streptomyces sp. (strain A647P-2).
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomyces.
 RN [1]
 RP SEQUENCE.
 RA Wakamiya T., Ueki Y., Shiba T., Kido Y., Motoki Y.;
 RT "The structure of ancovenin, a new peptide inhibitor of angiotensin I
 converting enzyme.";
 RL Tetrahedron Lett. 26:665-668(1985).

CC -!- FUNCTION: ACTS AS INHIBITOR OF ANGIOTENSIN I CONVERTING ENZYME.
 CC -!- SIMILARITY: STRUCTURAL SIMILARITY TO OTHER TYPE B LANTIBIOTICS.
 DR PIR; A61284; EWSMAN.
 KW Antibiotic; Lantibiotic.
 FT MOD_RES 4 4 D-ALANINE.
 FT MOD_RES 6 6 D-ALANINE (BONDED TO 19).
 FT MOD_RES 11 11 D-ABU (AMINOBTYRIC ACID).
 FT MOD_RES 18 18 D-ABU (AMINOBTYRIC ACID).
 FT MOD_RES 19 19 LYSINOALANINE (BONDED TO 6).
 FT THIOETH 1 18 ABU-S-CYS (METHYLLANTHIONINE).
 FT THIOETH 4 14 ALA-S-CYS (LANTHIONINE).
 FT THIOETH 5 11 ALA-S-CYS (METHYLLANTHIONINE).
 SQ SEQUENCE 19 AA; 2033 MW; F434299E2736286A CRC64;

Query Match 37.2%; Score 16; DB 1; Length 19;
 Best Local Similarity 50.0%; Pred. No. 2.8e+03;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 FGSLAF 8
 |||
 Db 7 FGPLTW 12

RESULT 24

ID MDH_BREDI STANDARD; PRT; 19 AA.
 AC P80542;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE MALATE DEHYDROGENASE (EC 1.1.1.37) (FRAGMENT).
 GN MDH.
 OS Brevundimonas diminuta (Pseudomonas diminuta).
 OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
 OC Brevundimonas.
 RN SEQUENCE.
 RC STRAIN=ATCC 11568;
 RX MEDLINE; 97334132.
 RA Charnock C.;
 RT "Structural studies of malate dehydrogenases (MDHs): MDHs in
 RT Brevundimonas species are the first reported MDHs in Proteobacteria
 RT which resemble lactate dehydrogenases in primary structure.";
 RL J. Bacteriol. 179:4066-4070(1997).
 CC -!- CATALYTIC ACTIVITY: L-MALATE + NAD(+) = OXALOACETATE + NADH.
 CC -!- SIMILARITY: BELONGS TO THE LDH FAMILY. MDH SUBFAMILY.
 DR INTERPRO: IPR001252; -.
 DR PROSITE; PS00068; MDH; PARTIAL.
 KW Oxidoreductase; Tricarboxylic acid cycle; NAD.
 FT NON_TER 19 19
 SQ SEQUENCE 19 AA; 1709 MW; 3B643277AB542F23 CRC64;

Query Match 37.2%; Score 16; DB 1; Length 19;
 Best Local Similarity 66.7%; Pred. No. 2.8e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 IFGSLA 7
 |||
 Db 13 IGGTLA 18

RESULT 25

ID MDH_BREVE STANDARD; PRT; 19 AA.
 AC P80543;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE MALATE DEHYDROGENASE (EC 1.1.1.37) (FRAGMENT).
 GN MDH.
 OS Brevundimonas vesicularis (Pseudomonas vesicularis).

OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
 OC Brevundimonas.
 RN SEQUENCE.
 RP STRAIN=ATCC 11426;
 RX MEDLINE; 97334132.
 RA Charnock C.;
 RT "Structural studies of malate dehydrogenases (MDHs): MDHs in
 RT Brevundimonas species are the first reported MDHs in Proteobacteria
 RT which resemble lactate dehydrogenases in primary structure.";
 RL J. Bacteriol. 179:4066-4070(1997).
 CC -!- CATALYTIC ACTIVITY: L-MALATE + NAD(+) = OXALOACETATE + NADH.
 CC -!- SIMILARITY: BELONGS TO THE LDH FAMILY. MDH SUBFAMILY.
 DR INTERPRO: IPR001252; -.
 DR PROSITE; PS00068; MDH; PARTIAL.
 KW Oxidoreductase; Tricarboxylic acid cycle; NAD.
 FT NON_TER 19 19
 SQ SEQUENCE 19 AA; 1709 MW; 3B643277AB542F23 CRC64;

Query Match 37.2%; Score 16; DB 1; Length 19;
 Best Local Similarity 66.7%; Pred. No. 2.8e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 IFGSLA 7
 |||
 Db 13 IGGTLA 18

Search completed: November 14, 2000, 11:57:08
 Job time: 15 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 14, 2000, 11:56:53 : Search time 13.23 Seconds
(without alignments)
43.170 Million cell updates/sec

Title: US-09-277-074-10

Perfect score: 43

Sequence: 1 KIFGSLAFL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 182106 seqs, 63460219 residues

Total number of hits satisfying chosen parameters: 3930

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_65.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	26	60.5	17	2 PA0004	plastocyanin - Ara
2	21	48.8	20	2 B60365	chymotrypsin inhib
3	21	48.8	20	2 A60365	trypsin inhibitor
4	20	46.5	16	2 A48839	T-cell receptor al
5	19	44.2	9	2 PT0225	Ig heavy chain CDR
6	19	44.2	10	2 S06964	hypothetical prote
7	19	44.2	12	2 A37933	Ig lambda chain J
8	19	44.2	14	2 B61597	cytochrome P450 AL
9	19	44.2	17	2 S71864	glutathione transf
10	19	44.2	17	2 S40530	neurone protein -
11	19	44.2	17	2 PH1312	Ig heavy chain DJ
12	19	44.2	18	2 JS0647	pheromotropin -
13	19	44.2	20	2 PU0033	aldose 1-epimerase
14	18	41.9	11	2 A35594	buccalin - Callifor
15	18	41.9	14	2 B39111	Ig heavy chain V r
16	18	41.9	14	2 A59018	Mucl enhancer bind
17	18	41.9	15	2 PC4213	bphB protein - Com
18	18	41.9	19	1 EMSMCN	cinnamycin - Strept
19	17	39.5	8	2 PC4373	telomeric and tetr
20	17	39.5	11	2 A57458	gene Gax protein -
21	17	39.5	12	2 S47393	T-cell antigen rec
22	17	39.5	15	2 PA0027	protein QA10006 -
23	17	39.5	15	2 PA0026	protein QA300027 -
24	17	39.5	15	2 B45115	peptidylprolyl iso
25	17	39.5	16	2 S24667	protein-tyrosine k
26	17	39.5	16	2 T14224	NADH dehydrogenase
27	17	39.5	17	2 S50901	chlorophyll a/b-bi
28	17	39.5	17	2 B42965	talain (glycosylate
29	17	39.5	17	2 I78870	gene Rbl protein -

30	17	39.5	18	2 I46653	T-cell receptor de
31	17	39.5	20	2 B61577	17.6k serine prote
32	16	37.2	7	2 I40504	hypothetical prote
33	16	37.2	9	3 PC7074	translation elonga
34	16	37.2	10	2 PT0038	glutathione transf
35	16	37.2	10	2 PT0230	Ig heavy chain CDR
36	16	37.2	11	2 D42965	talain - chicken (f
37	16	37.2	11	2 S57575	T cell receptor V-
38	16	37.2	12	2 PA0098	ribosomal protein
39	16	37.2	12	2 PT0257	Ig heavy chain CRD
40	16	37.2	12	2 D20907	Ig kappa-1 chain J
41	16	37.2	12	2 PH1457	T-cell receptor be
42	16	37.2	13	2 S03063	Ig lambda chain J
43	16	37.2	13	2 PH1772	T cell receptor al
44	16	37.2	13	2 S57567	T cell receptor V-
45	16	37.2	13	2 PH0796	T-cell receptor al

ALIGNMENTS

RESULT 1

PA0004

plastocyanin - Arabidopsis thaliana (fragment)

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 18-Nov-1994 #sequence_revision 06-Jan-1995 #text_change 15-Mar-1996

C:Accession: PA0004

R:Kano, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.

submitted to JIPID, July 1994

A:Description: Separation and characterization of Arabidopsis proteins by two-dimensi

A:Reference number: PA0001

A:Accession: PA0004

A:Molecule type: protein

A:Residues: 1-17 <KAM>

A:Experimental source: stem

C:Superfamily: plastocyanin

C:Keywords: copper; electron transfer

Query Match 60.5%; Score 26; DB 2; Length 17;
Best Local Similarity 83.3%; Pred. No. 37;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GSLAFL 9

Db 10 GSLAFI 15

RESULT 2

B60365

chymotrypsin inhibitor 2 - tobacco hornworm (fragment)

C:Species: Manduca sexta (tobacco hornworm)

C:Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 03-Feb-1994

C:Accession: B60365

R:Kanost, M.R.

Insect Biochem. 20, 141-147, 1990

A:Title: Isolation and Characterization of four serine proteinase inhibitors (serpins

A:Reference number: A60365

A:Accession: B60365

A:Molecule type: protein

A:Residues: 1-20 <KAM>

C:Keywords: hemolymph; monomer; serine proteinase inhibitor

Query Match 48.8%; Score 21; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 4.9e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 IFGSLAFL 9

Db 9 LHGSLYFI 16

RESULT 3
A0365
trypsin inhibitor - tobacco hornworm (fragment)
C:Species: Manduca sexta (tobacco hornworm)
C:Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 03-Feb-1994
C:Accession: A0365
R:Kano, M.R.
Insect Biochem. 20, 141-147, 1990
A:Title: Isolation and characterization of four serine proteinase inhibitors (serpins)
A:Reference number: A0365
A:Accession: A0365
A:Molecule type: protein
A:Residues: 1-20 <KAN>
C:Keywords: hemolymph; monomer; serine proteinase inhibitor

Query Match 48.8%; Score 21; DB 2; Length 20;
Best Local Similarity 66.7%; Pred. No. 4.9e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 GSLAFL 9
| | | | |
DB 11 GHLAFI 16

RESULT 4
A48839
T-cell receptor alpha chain V-N-J region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997
C:Accession: A48839
R:Katz, J.D.; Wang, B.; Haskins, K.; Benoist, C.; Mathis, D.
Cell 74, 1089-1100, 1993
A:Title: Following a diabetogenic T cell from genesis through pathogenesis.
A:Reference number: A48839; MUID:94006520
A:Accession: A48839
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-16 <KAT>
A:Experimental source: NOD, transgenic, diabetogenic T cell clone BDC2.5
A:Note: sequence extracted from NCBI backbone (NCBIP:138465)
C:Keywords: T-cell receptor

Query Match 46.5%; Score 20; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IFGS 5
| | | |
DB 12 IFGS 15

RESULT 5
PT0225
Ig heavy chain CDR3 region (clone 1-103) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0225
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A:Reference number: PT0222; MUID:91108337
A:Accession: PT0225
A:Molecule type: DNA
A:Residues: 1-9 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotrimer; immunoglobulin

Query Match 44.2%; Score 19; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.8e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 IFGSLA 7
| | | | |
DB 2 MFGGMA 7

RESULT 6
S06964
hypothetical protein (nifa 5' region) - Rhizobium leguminosarum (fragment)
C:Species: Rhizobium leguminosarum
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 08-Oct-1999
C:Accession: S06964
R:Roelivink, P.W.; Hontelez, J.G.J.; van Kammen, A.; van den Bos, R.C.
Mol. Microbiol. 3, 1441-1447, 1989
A:Title: Nucleotide sequence of the regulatory nifa gene of Rhizobium leguminosarum P
A:Reference number: S06964; MUID:90136072
A:Accession: S06964
A:Molecule type: DNA
A:Residues: 1-10 <ROE>
A:Cross-references: EMBL:X17073; NID:g46208; PIDN:CAA34923.1; PID:g809748

Query Match 44.2%; Score 19; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 6.4e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 FGSLAF 8
| | | | |
DB 4 FGVLKP 9

RESULT 7
A37933
Ig lambda chain J region - sheep (fragment)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 26-Jul-1991 #sequence_revision 26-Jul-1991 #text_change 05-Nov-1999
C:Accession: A37933
R:Reynaud, C.A.; Mackay, C.R.; Mueller, R.G.; Weill, J.C.
Cell 64, 995-1005, 1991
A:Title: Somatic generation of diversity in a mammalian primary lymphoid organ: the s
A:Reference number: A37933; MUID:91160063
A:Accession: A37933
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-12 <REV>
A:Cross-references: GB:M60440; NID:9165946; PIDN:AAA31550.1; PID:g552425
C:Keywords: heterotrimer; immunoglobulin

Query Match 44.2%; Score 19; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 7.7e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IFGS 5
| | | |
DB 2 VFCS 5

RESULT 8
B61597
cytochrome P450 AL-2 - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
C:Accession: B61597
R:Shimeno, H.; Toda, A.; Ogata, S.; Nagamatsu, A.
Drug Metab. Dispos. 19, 291-297, 1991
A:Title: Purification and aminopyrine monooxygenase activity of liver microsomal cyto
A:Reference number: A61597; MUID:91292910
A:Accession: B61597
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-14 <SHI>

Query Match 44.2%; Score 19; DB 2; Length 14;
 Best Local Similarity 80.0%; Pred. No. 9e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 SLAFL 9
 |||||
 DB 6 SLSEFL 10

RESULT 9
 S71864
 glutathione transferase (EC 2.5.1.18) class alpha 6a - pig (fragment)
 N:Alternate names: glutathione S-transferase class alpha 6a
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-May-1999
 C:Accession: S71864
 R:Rouimi, P.; Anglade, P.; Debrauwer, L.; Tulliez, J.
 Biochem. J. 317, 879-884, 1996
 A:Title: Characterization of pig liver glutathione S-transferases using HPLC-electrospray
 A:Reference number: S71864; MUID:96332484
 A:Accession: S71864
 A:Molecule type: protein
 A:Residues: 1-17 <R0U>
 A:Experimental source: liver; cytosolic
 C:Comment: At least five species-independent classes of cytosolic glutathione transferase
 s mitochondrial form are known.
 C:Complex: dimer
 C:Function:
 A:Description: catalyzes the nucleophilic conjugation of intracellular glutathione to a
 A:Pathway: detoxification; xenobiotics metabolism
 A:Note: increased hydrophilicity of GSH-conjugates facilitates their further metabolism
 es of damage
 C:Superfamily: glutathione transferase
 C:Keywords: dimer; transferase

Query Match 44.2%; Score 19; DB 2; Length 17;
 Best Local Similarity 80.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GSLAF 8
 |||||
 DB 2 GSLLF 6

RESULT 10
 S40530
 aleurone protein - barley
 C:Species: Hordeum vulgare (barley)
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 11-Jan-2000
 C:Accession: S40530
 R:Yupsanis, T.; Burgess, S.R.; Jackson, P.J.; Shewry, P.R.
 J. Exp. Bot. 41, 385-392, 1990
 A:Title: Characterization of the major protein component from aleurone cells of barley
 A:Reference number: S40530
 A:Accession: S40530
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-17 <YUP>
 C:Superfamily: glycinin

Query Match 44.2%; Score 19; DB 2; Length 17;
 Best Local Similarity 42.9%; Pred. No. 1.1e+03;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 IFGSLAF 8
 |||||
 DB 11 VFGPRSF 17

RESULT 11

PH1312
 Ig heavy chain DJ region (clone C68-105) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C:Accession: PH1312
 R:Wasserman, R.; Gallili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
 J. Exp. Med. 176, 1577-1581, 1992
 A:Title: Predominance of fetal type DJH joining in young children with B precursor ly
 A:Reference number: PH1302; MUID:93094761
 A:Accession: PH1312
 A:Molecule type: DNA
 A:Residues: 1-17 <WAS>
 C:Keywords: heterotetramer; immunoglobulin

Query Match 44.2%; Score 19; DB 2; Length 17;
 Best Local Similarity 37.5%; Pred. No. 1.1e+03;
 Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 IFGSLAF 9
 |||||
 DB 1 IFGVVIVI 8

RESULT 12
 JS0647
 pheromonotropin - armyworm (Pseudaletia separata)
 C:Species: Pseudaletia separata
 C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 11-Jul-1997
 C:Accession: JS0647
 R:Matsumoto, S.; Fonagy, A.; Kurihara, M.; Uchiumi, K.; Nagamine, T.; Chijimatsu, M.;
 Biochem. Biophys. Res. Commun. 182, 534-539, 1992
 A:Title: Isolation and primary structure of a novel pheromonotropic neuropeptide stru
 A:Reference number: JS0647; MUID:92134266
 A:Accession: JS0647
 A:Molecule type: protein
 A:Residues: 1-18 <MAT>
 C:Keywords: amidated carboxyl end
 F:18/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 44.2%; Score 19; DB 2; Length 18;
 Best Local Similarity 37.5%; Pred. No. 1.2e+03;
 Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 KIFGSLAF 8
 |||||
 DB 7 KVFNVEF 14

RESULT 13
 PU0033
 aldose 1-epimerase (EC 5.1.3.3) - pig (fragment)
 N:Alternate names: mutarotase
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
 C:Accession: PU0033
 R:Nakamura, T.; Kinoshita, T.; Kitazawa, S.; Kimura, A.; Chiba, S.
 Biosci. Biotechnol. Biochem. 57, 1772-1774, 1993
 A:Title: Structure determination of N-terminal-blocked peptide from hog kidney aldose
 A:Reference number: PU0033; MUID:94080039
 A:Accession: PU0033
 A:Molecule type: protein
 A:Residues: 1-20 <NAK>
 A:Experimental source: kidney
 C:Keywords: acetylated amino end; isomerase
 F:1/Modified site: acetylated amino end (Val) #status experimental

Query Match 44.2%; Score 19; DB 2; Length 20;
 Best Local Similarity 60.0%; Pred. No. 1.3e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 IFGSL 6
:|:|
Db 7 VFGDL 11

RESULT 14

buccalin - California sea hare
C:Species: Aplysia californica (California sea hare)
C:Date: 14-Sep-1990 #sequence_revision 14-Sep-1990 #text_change 24-Jun-1993
C:Accession: A35594
R:Cropper, E.C.; Miller, M.W.; Tenenbaum, R.; Kolks, M.A.G.; Kupfermann, I.; Weiss, K.R.
Proc. Natl. Acad. Sci. U.S.A. 85, 6177-6181, 1988
A:Title: Structure and action of buccalin: a modulatory neuropeptide localized to an ide
A:Reference number: A35594; MUID:88320404
A:Accession: A35594
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-11 <CRO>

Query Match 41.9%; Score 18; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SLAF 8
:|:|:|
Db 4 SLAF 7

RESULT 15

B39111
Ig heavy chain V region - Pacific hagfish (fragment)
C:Species: Eptatretus stoutii (Pacific hagfish)
C:Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 16-Aug-1996
C:Accession: B39111
R:Varner, J.; Neame, P.; Litman, G.W.
Proc. Natl. Acad. Sci. U.S.A. 88, 1746-1750, 1991
A:Title: A serum heterodimer from hagfish (Eptatretus stoutii) exhibits structural simil
A:Reference number: A39111; MUID:91156684
A:Accession: B39111
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-14 <VAR>
C:Keywords: heterotetramer; immunoglobulin

Query Match 41.9%; Score 18; DB 2; Length 14;
Best Local Similarity 60.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 FGSLA 7
:|:|
Db 4 YGNLA 8

RESULT 16

A59018
MUC1 enhancer binding protein 70K chain MUCLEBP-70 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 08-May-1998
C:Accession: A59018
R:Abe, M.; Smith, C.J.; Larson, C.J.
submitted to the Protein Sequence Database, May 1998
A:Description: Involvement of "Ku-like" proteins in the transcription of MUC1/DF3, a bra
A:Reference number: A59018
A:Accession: A59018
A:Molecule type: protein
A:Residues: 1-14 <ABE>
A:Experimental source: breast cancer cell line MCF-7
A:Note: 3-Val was also found
C:Keywords: DNA binding; heterodimer

Query Match 41.9%; Score 18; DB 2; Length 14;
Best Local Similarity 60.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIFGS 5
:|:|
Db 3 QIYGS 7

RESULT 17

bphB protein - Comamonas testosteroni (fragment)
C:Species: Comamonas testosteroni
C:Date: 17-Dec-1996 #sequence_revision 21-Jan-1997 #text_change 08-Oct-1999
C:Accession: PC4213
R:Sylvestre, M.; Sirols, M.; Hurtubise, Y.; Bergeron, J.; Ahmed, D.; Shareck, F.; Bar
Gene 174, 195-202, 1996
A:Title: Sequencing of Comamonas testosteroni strain B-356-biphenyl/chlorobiphenyl di
A:Reference number: JC4993; MUID:97045812
A:Accession: PC4213
A:Molecule type: DNA
A:Residues: 1-15 <SVL>
A:Cross-references: GB:U47637; NID:gl245151; PIDN:AAC44530.1; PID:gl245156
A:Experimental source: strain B-356
C:Genetics:
A:Gene: bphB

Query Match 41.9%; Score 18; DB 2; Length 15;
Best Local Similarity 33.3%; Pred. No. 1.6e+03;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 KIFGSLAFL 9
:|:|:|
Db 2 KLTGEVALI 10

RESULT 18

ENSMCN
cinnamycin - Streptovorticillium cinnamoneum
N:Alternate names: lanthiopeptin; lantibiotic Ro 09-0198
C:Species: Streptovorticillium cinnamoneum
C:Date: 30-Sep-1993 #sequence_revision 12-May-1994 #text_change 07-May-1999
C:Accession: A45767
R:Naruse, N.; Tenmyo, O.; Tomita, K.; Konishi, M.; Miyaki, T.; Kawaguchi, H.; Fukase,
J. Antibiot. 42, 837-845, 1989
A:Title: Lanthiopeptin, a new peptide antibiotic. Production, isolation and properle
A:Reference number: A45767; MUID:89291558
A:Accession: A45767
A:Molecule type: protein
A:Residues: 1-19 <NAR>
R:Wakamiya, T.; Fukase, K.; Naruse, N.; Konishi, M.; Shiba, T.
Tetrahedron Lett. 29, 4771-4772, 1988
A:Title: Lanthiopeptin, a new peptide effective against Herpes simplex virus: structu
A:Reference number: A53359
A:Contents: annotation; strain L337-2
C:Superfamily: cinnamycin precursor
C:Keywords: antibiotic; beta-hydroxyaspartic acid; lanthionine
F:1-18/Cross-link: (2S,3S,6R)-3-methyl-lanthionine (Cys-Thr) #status experimental
F:4-14/Cross-link: sn-(2S,6R)-lanthionine (Ser-Cys) #status experimental
F:5-11/Cross-link: (2S,3S,6R)-3-methyl-lanthionine (Cys-Thr) #status experimental
F:6-19/Cross-link: (2X1,9S)-lysinoalanine (Ser-Lys) #status experimental
F:15/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental

Query Match 41.9%; Score 18; DB 1; Length 19;
Best Local Similarity 42.9%; Pred. No. 2e+03;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 FGSLAFL 9
:|:|
Db 7 FGPFTFV 13

RESULT 19

PC4373
telomeric and tetraplex DNA binding protein qTBP42 III - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 28-Oct-1997 #sequence_revision 28-Oct-1997 #text_change 07-May-1999
C:Accession: PC4373
R:Sarig, G.; Weisman-Shomer, P.; Fry, M.
Biochem. Biophys. Res. Commun. 237, 617-623, 1997
A:Title: Telomeric and tetraplex DNA binding properties of qTBP42: A homologue of the C
A:Reference number: PC4371; MUID:97445086
A:Accession: PC4373
A:Molecule type: protein
A:Residues: 1-8 <SAR>
C:Comment: This protein binds either strand of the telomeric DNA as well as unimolecular
F:1-4/Domain: RNPI #status predicted <RNP>

Query Match 39.5%; Score 17; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.8e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 FGSLAF 8
||:|
Db 2 FGFILF 7

RESULT 20

A57458
gene Gax protein - mouse (fragment)
C:Species: Mus sp. (mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 15-Oct-1999
C:Accession: A57458
R:Andres, V.; Fisher, S.; Wearsch, P.; Walsh, K.
Mol. Cell. Biol. 15, 4272-4281, 1995
A:Title: Regulation of Gax homeobox gene transcription by a combination of positive fact
A:Reference number: A57458; MUID:95349593
A:Accession: A57458
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-11 <RES>
A:Cross-references: GB:S79168; NID:g1050991
C:Genetics:
A:Gene: Gax
C:Superfamily: unassigned homeobox proteins; homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match 39.5%; Score 17; DB 2; Length 11;
Best Local Similarity 60.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 IFGSL 6
||:|
Db 5 LFGCL 9

RESULT 21

S47393
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47393
R:Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A*0201 restricted recognition of influenza A is dominated by T c
A:Reference number: S47355
A:Accession: S47393
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-12 <LEH>
A:Cross-references: EMBL:235670; NID:g527445; PIDN:CAA84739.1; PID:g527446

C:Keywords: T-cell receptor

Query Match 39.5%; Score 17; DB 2; Length 12;
Best Local Similarity 57.1%; Pred. No. 2e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 IFGSLAF 8
||:|
Db 5 IVGTEAF 11

RESULT 22

PA0027
protein QAI00006 - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
C:Accession: PA0027
R:Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JIPID, July 1994
A:Description: Separation and characterization of Arabidopsis proteins by two-dimensi
A:Reference number: PA0001
A:Accession: PA0027
A:Molecule type: protein
A:Residues: 1-15 <KAM>
A:Experimental source: callus

Query Match 39.5%; Score 17; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 2.5e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIFG 4
||:|
Db 3 KVYG 6

RESULT 23

PA0026
protein QA300027 - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
C:Accession: PA0026
R:Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JIPID, July 1994
A:Description: Separation and characterization of Arabidopsis proteins by two-dimensi
A:Reference number: PA0001
A:Accession: PA0026
A:Molecule type: protein
A:Residues: 1-15 <KAM>
A:Experimental source: leaf

Query Match 39.5%; Score 17; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 2.5e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIFG 4
||:|
Db 3 KVYG 6

RESULT 24

B45115
peptidylprolyl isomerase (EC 5.2.1.8) FKBP51 - human (fragment)
N:Alternate names: FK506-binding protein FKBP51; peptidylprolyl cis-trans isomerase F
C:Species: Homo sapiens (man)
C:Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 16-Feb-1997
C:Accession: B45115
R:Wiederrecht, G.; Hung, S.; Chan, H.K.; Marcy, A.; Martin, M.; Calaycay, J.; Boulton
J. Biol. Chem. 267, 21753-21760, 1992
A:Title: Characterization of high molecular weight FK-506 binding activities reveals
A:Reference number: A45115; MUID:93016131

A:Accession: B45115
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <WIE>
A:Experimental source: JURKAT cells
A:Note: sequence extracted from NCBI backbone (NCBIP:116748)
C:Keywords: cis-trans-isomerase; cyclosporin A binding

Query Match 39.5%; Score 17; DB 2; Length 15;
Best Local Similarity 60.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 SLAPL 9
|:|:|
Db 4 SIAYL 8

RESULT 25
S24667
protein-tyrosine kinase (EC 2.7.1.112) kit - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 03-Mar-1994 #sequence_revision 13-Mar-1997 #text_change 04-Feb-2000
C:Accession: S24667
R:Sortentino, V.
submitted to the EMBL Data Library, May 1992
A:Reference number: S24666
A:Accession: S24667
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-16 <SOR>
A:Cross-references: EMBL:X65998; NID:g50433; PIDN:CAA46799.1; PID:g50434
C:Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase

Query Match 39.5%; Score 17; DB 2; Length 16;
Best Local Similarity 60.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 SLAPL 9
|:|:|
Db 8 AMAFL 12

Search completed: November 14, 2000, 11:58:05
Job time: 72 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 14, 2000, 11:56:53 ; Search time 17.04 Seconds
(without alignments)
49.317 Million cell updates/sec

Title: US-09-277-074-10
Perfect score: 43
Sequence: 1 KIFGSLAFL 9

Scoring table: BLOSUM62
Gapop 10.0 , Capext 0.5

Searched: 297973 seqs, 93374136 residues

Total number of hits satisfying chosen parameters: 4186

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_14.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	25	58.1	18	2 Q9RQ90	Q9RQ90 buchnera ap
2	22	51.2	18	2 O06514	O06514 escherichia
3	22	51.2	20	2 Q9R411	Q9R411 bordetella
4	21	48.8	16	13 P82391	P82391 litoria aur
5	20	46.5	15	11 Q9R0X7	Q9R0X7 mus musculus
6	20	46.5	16	13 P82388	P82388 litoria aur
7	20	46.5	16	13 P82389	P82389 litoria aur
8	20	46.5	16	13 P82392	P82392 litoria ran
9	20	46.5	20	2 Q32710	Q32710 klebsiella
10	19	44.2	10	2 Q52837	Q52837 rhizobium 1
11	19	44.2	18	6 Q95305	Q95305 sus scrofa
12	19	44.2	18	13 P82068	P82068 litoria gen
13	18	41.9	10	12 Q9QKJ0	Q9QKJ0 human immun
14	18	41.9	12	12 Q89243	Q89243 woodchuck h
15	18	41.9	15	8 Q9T2G9	Q9T2G9 solanum tub
16	18	41.9	16	10 O82403	O82403 fragaria ve
17	18	41.9	16	13 P82390	P82390 litoria aur
18	18	41.9	17	5 Q26832	Q26832 trypanosoma
19	18	41.9	17	5 Q9VVG5	Q9VVG5 drosophila

20	18	41.9	17	13 P82394	P82394 litoria ran
21	18	41.9	17	13 P82395	P82395 litoria ran
22	18	41.9	18	6 Q97668	Q97668 equus cabal
23	18	41.9	18	8 Q9T2G8	Q9T2G8 solanum tub
24	18	41.9	19	4 Q9UMW9	Q9UMW9 homo sapien
25	18	41.9	19	12 Q73129	Q73129 human lmmun
26	18	41.9	20	2 Q9R496	Q9R496 pseudomonas
27	18	41.9	20	8 Q9T2K6	Q9T2K6 cucurbita m
28	18	41.9	20	12 Q9PXE4	Q9PXE4 foot-and-mo
29	17.5	40.7	15	8 P92818	P92818 paralichthy
30	17	39.5	12	7 Q77879	Q77879 oreochromis
31	17	39.5	13	7 Q19789	Q19789 homo sapien
32	17	39.5	13	11 Q62354	Q62354 mus musculu
33	17	39.5	15	4 Q9UQA5	Q9UQA5 homo sapien
34	17	39.5	15	8 Q9T2V7	Q9T2V7 homo sapien
35	17	39.5	16	1 Q9UWK4	Q9UWK4 methanobact
36	17	39.5	16	6 Q62810	Q62810 equus cabal
37	17	39.5	16	8 P92070	P92070 euhadra her
38	17	39.5	16	13 P82393	P82393 litoria ran
39	17	39.5	17	2 Q9R5X6	Q9R5X6 mycoplasma.
40	17	39.5	17	4 Q92727	Q92727 homo sapien
41	17	39.5	17	4 Q9UJH1	Q9UJH1 homo sapien
42	17	39.5	17	8 Q9T2H4	Q9T2H4 spinacia ol
43	17	39.5	17	12 Q9QPC8	Q9QPC8 tomato yell
44	17	39.5	18	4 Q16028	Q16028 homo sapien
45	17	39.5	18	7 Q9TNP1	Q9TNP1 mus sp. mhc

ALIGNMENTS

RESULT 1

Q9RQ90 PRELIMINARY; PRT; 18 AA.
AC Q9RQ90;
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
DE HYPOTHETICAL 1.9 KDA PROTEIN (FRAGMENT).
OS Buchnera aphidicola.
OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 20022990.
RA Clark M.A., Moran N.A., Baumann P.;
RT "Sequence evolution in bacterial endosymbionts having extreme base
RT compositions.";
RL Mol. Biol. Evol. 16:1586-1598(1999).
DR EMBL; AF129281; AAF13768.1; -.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 18 AA; 1885 MW; 96F90D72D88F4425 CRC64;

Query Match 58.1%; Score 25; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIFGS 5

Db 3 KIFGS 7

RESULT 2

O06514 PRELIMINARY; PRT; 18 AA.
ID O06514
AC O06514;
DT 01-JUL-1997 (TremBLrel. 04, Created)
DT 01-JUL-1997 (TremBLrel. 04, Last sequence update)
DE DNA, MOSAIC MERCURY RESISTANCE TRANSPOSABLE ELEMENT
DE (MER-OPERON)1040 BP (FRAGMENT).
GN MERP.

```

OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-CH210; TRANSPOSON-TN5059;
RC MEDLINE; 97303088.
RA Nikiforov V., Kholodii G., Minakhin L., Gorlenko Z., Kalyaeva E.,
RA Mindlin S., Nikiforov V.;
RT "Intercontinental spread of promiscuous mercury-resistance transposons
in environmental bacteria.";
RL Mol. Microbiol. 24:321-329(1997).
DR EMBL; Y09026; CAA70241.1; -.
FT NON_TER 18
SQ SEQUENCE 18 AA; 1899 MW; 484A2D7197814DF9 CRC64;

Query Match 51.2%; Score 22; DB 2; Length 18;
Best Local Similarity 57.1%; Pred. No. 5.7e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KIFGSLAFL 7
DB 3 KLFAALA 9
I: I: I: I:

RESULT 3
Q9R411 PRELIMINARY; PRT; 20 AA.
AC Q9R411;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 92 KDA OUTER MEMBRANE PROTEIN (FRAGMENT).
OS Bordetella pertussis.
OC Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
OC Bordetella.
RN [1]
RP SEQUENCE.
RX Hamstra H.J., Kuipers B., Schijf-Evers D., Loggen H.G., Poolman J.T.;
RT "The purification and protective capacity of Bordetella pertussis
outer membrane proteins.";
RL Vaccine 13:747-752(1995).
SQ SEQUENCE 20 AA; 1874 MW; A41702F66A87C888 CRC64;

Query Match 51.2%; Score 22; DB 2; Length 20;
Best Local Similarity 55.6%; Pred. No. 6.3e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 KIFGSLAFL 9
DB 8 RIDGGAFL 16
I: I: I: I: I: I: I: I: I: I:

RESULT 4
P82391 PRELIMINARY; PRT; 16 AA.
AC P82391;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE AUREIN 2.4/2.4.1.
OS Litoria aurea (Australian frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Litoria.
RN [1]
RP SEQUENCE.
RX Rozek T., Wegener K.L., Bowie J.H., Oliver I.N., Carver J.A.,
RA Wallace J.C., Tyler M.J.;
RT "The antibiotic and anticancer aurein peptides from the Australian
bell frogs Litoria aurea and Litoria raniformis.";
RL Eur. J. Biochem. 0:0-0(2000).
CC -1- FUNCTION: AUREIN 2.1 HAS ANTIMICROBIAL AND ANTICANCER ACTIVITY.
KW Amidation; Antibiotic.
FT PEPTIDE 3 16
MOD_RES 16 16
AMIDATION.

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RT bell frogs Litoria aurea and Litoria raniformis.";
RL Eur. J. Biochem. 0:0-0(2000).
CC -1- FUNCTION: AUREIN 2.4 HAS ANTIMICROBIAL AND ANTICANCER ACTIVITY.
KW Amidation; Antibiotic.
FT PEPTIDE 3 16
MOD_RES 16 16
SQ SEQUENCE 16 AA; 1630 MW; 1D87980438AAE2F9 CRC64;

Query Match 48.8%; Score 21; DB 13; Length 16;
Best Local Similarity 44.4%; Pred. No. 8e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 KIFGSLAFL 9
DB 8 KVVGTIAGL 16
I: I: I: I: I: I: I: I: I: I:

RESULT 5
Q9R0X7 PRELIMINARY; PRT; 15 AA.
AC Q9R0X7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE ACTIVATED NOTCH1 ONCOPROTEIN (FRAGMENT).
GN NOTCH1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RA Lee J.S., Ishimoto A., Yanagawa S.I.;
RT "Murine leukemia provirus-mediated activation of the Notch1 gene: leads
to induction of HES-1 in a mouse T lymphoma cell line, DL-3.";
RL FEBS Lett. 455:276-280(1999).
DR EMBL; AJ238029; CAB40733.1; -.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1794 MW; C06FC27C9B6E307B CRC64;

Query Match 46.5%; Score 20; DB 11; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 IFGSLAFL 9
DB 3 IRGSIVIL 10
I: I: I: I: I: I: I: I: I: I:

RESULT 6
P82388 PRELIMINARY; PRT; 16 AA.
AC P82388;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE AUREIN 2.1/2.1.1.
OS Litoria raniformis, and Litoria aurea (Australian frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Litoria.
RN [1]
RP SEQUENCE.
RX Rozek T., Wegener K.L., Bowie J.H., Oliver I.N., Carver J.A.,
RA Wallace J.C., Tyler M.J.;
RT "The antibiotic and anticancer aurein peptides from the Australian
bell frogs Litoria aurea and Litoria raniformis.";
RL Eur. J. Biochem. 0:0-0(2000).
CC -1- FUNCTION: AUREIN 2.1 HAS ANTIMICROBIAL AND ANTICANCER ACTIVITY.
KW Amidation; Antibiotic.
FT PEPTIDE 3 16
MOD_RES 16 16
AMIDATION.

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SQ SEQUENCE 16 AA; 1616 MW; 1D9A5DADB4D240F9 CRC64;

Query Match 46.5%; Score 20; DB 13; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 FGSL 6
Db 13 FGSL 16

RESULT 7

ID P82389 PRELIMINARY; PRT; 16 AA.
AC P82389;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE AUREIN 2.2/2.1.
OS Litoria aurea (Australian frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Litoria.
RN [1]
RA SEQUENCE.
RA Rozek T., Wegener K.L., Bowie J.H., Olver I.N., Carver J.A.,
RA Wallace J.C., Tyler M.J.;
RT "The antibiotic and anticancer aurein peptides from the Australian
RT bell frogs Litoria aurea and Litoria raniformis.";
RL Eur. J. Biochem. 0:0-0(2000).
CC -I- FUNCTION: AUREIN 2.2 HAS ANTIMICROBIAL AND ANTICANCER ACTIVITY.
KW Amidation; Antibiotic.
FT PEPTIDE 3 16 AUREIN 2.2.1.
FT MOD.RES 16 16 AMIDATION.
SQ SEQUENCE 16 AA; 1616 MW; 1D9A5DA354DAE2F9 CRC64;

Query Match 46.5%; Score 20; DB 13; Length 16;
Best Local Similarity 44.4%; Pred. No. 1.3e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KIFGSLAFL 9
Db 8 KVGAGLSL 16

RESULT 8

ID P82392 PRELIMINARY; PRT; 16 AA.
AC P82392;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE AUREIN 2.5.
OS Litoria raniformis, and Litoria aurea (Australian frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Litoria.
RN [1]
RA SEQUENCE.
RA Rozek T., Wegener K.L., Bowie J.H., Olver I.N., Carver J.A.,
RA Wallace J.C., Tyler M.J.;
RT "The antibiotic and anticancer aurein peptides from the Australian
RT bell frogs Litoria aurea and Litoria raniformis.";
RL Eur. J. Biochem. 0:0-0(2000).
CC -I- FUNCTION: HAS ANTIMICROBIAL AND ANTICANCER ACTIVITY.
KW Amidation; Antibiotic.
FT MOD.RES 16 16 AMIDATION.
SQ SEQUENCE 16 AA; 1650 MW; 1D9A5DADB4DAE2F9 CRC64;

Query Match 46.5%; Score 20; DB 13; Length 16;

Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 FGSL 6
Db 13 FGSL 16

RESULT 9

ID O32710 PRELIMINARY; PRT; 20 AA.
AC O32710;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE YHHT PROTEIN (FRAGMENT).
CN YHHT.
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Klebsiella.
RN [1]
RA SEQUENCE FROM N.A.
RX MEDLINE: 97352552.
RA Hoenke S., Schmid M., Dimroth P.;
RT "Sequence of a gene cluster from Klebsiella pneumoniae encoding
RT malonate decarboxylase and expression of the enzyme in Escherichia
RT coli.";
RL Eur. J. Biochem. 246:530-538(1997).
DR EMBL: U95087; AAC45462.1; -.
FT NON_TER 1 1
SQ SEQUENCE 20 AA; 2108 MW; 86A17AAC8BF77BFA CRC64;

Query Match 46.5%; Score 20; DB 2; Length 20;
Best Local Similarity 80.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 SLAFL 9
Db 9 SLAFL 13

RESULT 10

ID Q52837 PRELIMINARY; PRT; 10 AA.
AC Q52837;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE FIXX PROTEIN (10 AA) (FRAGMENT).
OS Rhizobium leguminosarum.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
RN [1]
RA SEQUENCE FROM N.A.
RC STRAIN=PRE;
RX MEDLINE: 90136072.
RA Roelvink P.W., Hontelez J.G.J., Van Kammen A., van den Bos R.C.;
RT "Nucleotide sequence of the regulatory nifA gene of Rhizobium
RT leguminosarum PRE; transcriptional control sites and expression in
RT Escherichia coli.";
RL EMBL: X17073; CAA34923.1; -.
FT NON_TER 1 1
SQ SEQUENCE 10 AA; 1037 MW; 24A5593732C879C8 CRC64;

Query Match 44.2%; Score 19; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 FGSLAF 8
Db 11

Db 4 FGVLKF 9

RESULT 11

Q95305 ID Q95305 PRELIMINARY; PRT; 18 AA.
 AC Q95305;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE MITOCHONDRIAL PHOSPHATE CARRIER PROTEIN (FRAGMENT).
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 RN [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE=SMALL INTESTINE;
 RA Winteroe A.K., Fredholm M., Davies W.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z81168; CAB03553.1; -.
 KW Mitochondrion.
 FT NON_TER 18
 SQ SEQUENCE 18 AA; 1985 MW; 07DBDAC362B0ACD4 CRC64;

Query Match 44.2%; Score 19; DB 6; Length 18;
 Best Local Similarity 50.0%; Pred. No. 2.3e+03;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 IFGSLAFL 9

: | | | |

Db 1 MFSSVAHL 8

RESULT 12

P82068 ID P82068 PRELIMINARY; PRT; 18 AA.
 AC P82068;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE MACULATIN 2.1.
 OS Litoria genimaculata (Green-eyed tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoides; Hylidae;
 OC Litoria.
 RN [1]
 RN SEQUENCE, AND MASS SPECTROMETRY . S.T., Bowle J.H., Tyler M.J.,
 RA Rozek T., Waugh R.J., Steinborner S.T.,
 RA Wallace J.C.;
 RT "The maculatin peptide from the skin glands of the tree frog
 Litoria genimaculata. A comparison of the structures and
 RT antibacterial activities of maculatin 1.1 and caerin 1.1.";
 RL J. Pept. Sci. 4:111-115(1998).
 CC -1- FUNCTION: SHOWS ANTIBACTERIAL ACTIVITY AGAINST B.CEREUS,
 CC L.INNOCUA, M.LUTEUS, S.AUREUS, S.EPIDERMISAND S.UBERIS.
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
 CC -1- MASS SPECTROMETRY: MW=1878; METHOD=Fab.
 KW Amphibian skin; Amidation; Antibiotic.
 FT MOD_RES 18 18
 SQ SEQUENCE 18 AA; 1879 MW; 98A1F86BB4FACBBE CRC64;

Query Match 44.2%; Score 19; DB 13; Length 18;
 Best Local Similarity 42.9%; Pred. No. 2.3e+03;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KIFGSLA 7

: | | | |

Db 8 KVAGTIA 14

RESULT 13

Q95305 ID Q95305 PRELIMINARY; PRT; 18 AA.
 AC Q95305;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE MITOCHONDRIAL PHOSPHATE CARRIER PROTEIN (FRAGMENT).
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 RN [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE=SMALL INTESTINE;
 RA Winteroe A.K., Fredholm M., Davies W.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z81168; CAB03553.1; -.
 KW Mitochondrion.
 FT NON_TER 18
 SQ SEQUENCE 18 AA; 1985 MW; 07DBDAC362B0ACD4 CRC64;

Query Match 44.2%; Score 19; DB 6; Length 18;
 Best Local Similarity 50.0%; Pred. No. 2.3e+03;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 IFGSLAFL 9

: | | | |

Db 1 MFSSVAHL 8

Q90KJ0

ID Q90KJ0 PRELIMINARY; PRT; 10 AA.
 AC Q90KJ0;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=22202V3.1;
 RA Korber B., Van Dyke R., Wolinsky S., Popek E., Macken C., Widmayer S.,
 RA Bardequez A., Hansen C., Wiznia A., Luzuriaga K., Viscarello R.;
 RT "The Ariel project: a prospective cohort study of maternal-child
 RT transmission of human immunodeficiency virus type 1 in the era of
 RT maternal antiretroviral therapy.";
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF112548; AAF13326.1; -.
 KW Envelope protein.
 FT NON_TER 1
 SQ SEQUENCE 10 AA; 961 MW; 4EDD23640DDB1DD7 CRC64;

Query Match 41.9%; Score 18; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GSALA 7

: | | | |

Db 1 GSALA 4

RESULT 14

Q89243 ID Q89243 PRELIMINARY; PRT; 12 AA.
 AC Q89243;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last annotation update)
 DE CORE PROTEIN (FRAGMENT).
 OS Woodchuck hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=W64;
 RX MEDLINE; 87219879.
 RA Etienneble J., Moroy T., Trepo C., Tiollais P., Buendia M.A.;
 RT "Nucleotide sequence of the woodchuck hepatitis virus surface antigen
 RT mRNAs and the variability of three overlapping viral genes.";
 RL Gene 500:207-214(1986).
 DR EMBL; M15954; AAA69576.1; -.
 FT NON_TER 12
 SQ SEQUENCE 12 AA; 1388 MW; 21ABC172F2132B47 CRC64;

Query Match 41.9%; Score 18; DB 12; Length 12;
 Best Local Similarity 80.0%; Pred. No. 2.4e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KIFGS 5

: | | | |

Db 7 KEFGS 11

RESULT 15

Q9T2G9 ID Q9T2G9 PRELIMINARY; PRT; 15 AA.
 AC Q9T2G9;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)

```

DE CARBONIC ANHYDRASE (EC 4.2.1.1) (FRAGMENT).
OS Solanum tuberosum (potato).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; Asteridae; euasterids I; Solanales;
OC Solanaceae; Solanum.
RN [1]
RP SEQUENCE.
RX MEDLINE; 96327808.
RA Rumeau D., Guine S., Fina L., Gault N., Nicole M., Peltier G.;
RT "Subcellular distribution of carbonic anhydrase in Solanum tuberosum
L. leaves: characterization of two compartment-specific isoforms.";
RL Planta 199;79-88(1996).
SQ SEQUENCE 15 AA; 1647 MW; CA587063CDD32976 CRC64;

Query Match 41.9%; Score 18; DB 8; Length 15;
Best Local Similarity 80.0%; Pred. No. 3e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GSLAP 8
   :|||
Db 4 GSKAF 8

RESULT 16
O82403
ID O82403 PRELIMINARY; PRT; 16 AA.
AC O82403;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE ALCOHOL DEHYDROGENASE (EC 1.1.1.1) (ALDEHYDE REDUCTASE) (FRAGMENT).
GN ADH.
OS Fragaria vesca.
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; Rosidae; eurosids I; Rosales; Rosaceae;
OC Fragaria.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PAWTUCKAWAY;
RA Yu H., Davis T.M.;
RT "Genetic relationships among Fragaria species based on RAPDs and an
RT alcohol dehydrogenase (ADH) gene.";
RL Genome 0:0-0(1997).
CC -1- CATALYTIC ACTIVITY: AN ALCOHOL + NAD(+) = AN ALDEHYDE OR KETONE +
CC NADH.
CC -1- COFACTOR: ZINC OR IRON.
DR EMBL; AF000215; AAC36542.1; -.
KW Oxidoreductase.
FT NON_TER 1 1
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1666 MW; CEF73B5B28A4CA87 CRC64;

Query Match 41.9%; Score 18; DB 10; Length 16;
Best Local Similarity 75.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIFG 4
   :|||
Db 8 RIFG 11

RESULT 17
P82390
ID P82390 PRELIMINARY; PRT; 16 AA.
AC P82390;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE AUREIN 2.3.
OS Litorea aurea (Australian frog).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Litoria.
RN [1]
RP SEQUENCE.
RA Rozek T., Wegener K.L., Bowie J.H., Oliver I.N., Carver J.A.,
RA Wallace J.C., Tyler M.J.;
RT "The antibiotic and anticancer aurein peptides from the Australian
RT bell frogs Litorea aurea and Litoria raniformis.";
RL Eur. J. Biochem. 0:0-0(2000).
KW -1- FUNCTION: HAS ANTIMICROBIAL AND ANTICANCER ACTIVITY.
KW Amidation; Antibiotic.
FT MOD_RES 16 16
FT AMIDATION.
SQ SEQUENCE 16 AA; 1616 MW; 1D9A5DA424DAE2F9 CRC64;

Query Match 41.9%; Score 18; DB 13; Length 16;
Best Local Similarity 33.3%; Pred. No. 3.2e+03;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 KIFGSLAPL 9
   :|:|:|
Db 8 KVGAIGSL 16

RESULT 18
Q26832
ID Q26832 PRELIMINARY; PRT; 17 AA.
AC Q26832;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE (TATAT 1.2) VARIANT SURFACE GLYCOPROTEIN ELC GENE (FRAGMENT).
OS Trypanosoma brucei brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 86278091.
RA Brown K.H., Brentano S.T., Donelson J.E.;
RT "Mung bean nuclease cleaves preferentially at the boundaries of
RT variant surface glycoprotein gene transpositions in trypanosome DNA.";
RL J. Biol. Chem. 261:10352-10358(1986).
DR EMBL; M14020; AAA30305.1; -.
FT NON_TER 1 1
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1973 MW; 9E00FBD261B8FFBF CRC64;

Query Match 41.9%; Score 18; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LAFL 9
   :|||
Db 12 LAFL 15

RESULT 19
Q9VVG5
ID Q9VVG5 PRELIMINARY; PRT; 17 AA.
AC Q9VVG5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE CG7630 PROTEIN.
GN CG7630.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE; 20196006.

```

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Gallie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton C.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers J.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.D.G.,
 RA Abril J.F., Aghayani A., An H.-J., Andrews-Fianngoch C., Baldwin D.,
 RA Ballw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlike C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferliera S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.:
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 DR EMBL; AE003524; AAF49346.1; -
 DR FLYBASE; FBgn040793; CG7630.
 SQ SEQUENCE 17 AA; 1865 MW; F982197C175EBBA CRC64;

Query Match 41.9%; Score 18; DB 5; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SLAF 8
 ||||
 Db 5 SLAF 8

RESULT 20
 P82394
 ID P82394 PRELIMINARY; PRT; 17 AA.
 AC P82394;
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)
 DE AUREIN 3.1/3.1.1.2.
 OS Litoria raniformis, and Litoria aurea (Australian frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
 OC Litoria.
 RN [1]
 RP SEQUENCE.
 RA Rozek T., Wegener K.L., Bowie J.H., Oliver I.N., Carver J.A.,
 RA Wallace J.C., Tyler M.J.:
 RT "The antibiotic and anticancer aurein peptides from the Australian
 RT bell frogs *Litoria aurea* and *Litoria raniformis*.";
 RL Eur. J. Biochem. 0:0-0(2000).
 CC -|- FUNCTION: AUREIN 3.1 HAS ANTIMICROBIAL AND ANTICANCER ACTIVITY.
 CC -|- MISCELLANEOUS: AUREIN 3.1.1 IS NOT AMIDATED.

KW Amidation; Antibiotic.
 FT PEPTIDE 1 14 AUREIN 3.1.1.
 FT PEPTIDE 3 17 AUREIN 3.1.2.
 FT MOD_RES 17 17 AMIDATION.
 SQ SEQUENCE 17 AA; 1739 MW; F6AC17980428EAFD CRC64;
 Query Match 41.9%; Score 18; DB 13; Length 17;
 Best Local Similarity 57.1%; Pred. No. 3.4e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 KIFGSLA 7
 || | : |
 Db 8 KIAGHIA 14
 RESULT 21
 P82395
 ID P82395 PRELIMINARY; PRT; 17 AA.
 AC P82395;
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)
 DE AUREIN 3.2.
 OS Litoria raniformis, and Litoria aurea (Australian frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
 OC Litoria.
 RN [1]
 RP SEQUENCE.
 RA Rozek T., Wegener K.L., Bowie J.H., Oliver I.N., Carver J.A.,
 RA Wallace J.C., Tyler M.J.:
 RT "The antibiotic and anticancer aurein peptides from the Australian
 RT bell frogs *Litoria aurea* and *Litoria raniformis*.";
 RL Eur. J. Biochem. 0:0-0(2000).
 CC -|- FUNCTION: HAS ANTIMICROBIAL AND ANTICANCER ACTIVITY.
 KW Amidation; Antibiotic.
 FT MOD_RES 17 17 AMIDATION.
 SQ SEQUENCE 17 AA; 1769 MW; F6AC0A580428EAFD CRC64;

Query Match 41.9%; Score 18; DB 13; Length 17;
 Best Local Similarity 57.1%; Pred. No. 3.4e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KIFGSLA 7
 || | : |
 Db 8 KIAGHIA 14

RESULT 22
 O97668
 ID O97668 PRELIMINARY; PRT; 18 AA.
 AC O97668;
 DT 01-MAY-1999 (TRENBLrel. 10, Created)
 DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)
 DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)
 DE LACTOFERRIN (FRAGMENT).
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Brandon R.B., Giffard J.M., Bell T.K.:
 RT "Isolation of Equine Lactoferrin Gene."
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF102025; AAC77463.1; -
 DR HSSP; P24627; 1BLF.
 DR INTERPRO; IPR001156; -
 DR PFAM; PF00405; transferrin; 1.
 FT NON_TER 1
 FT NON_TER 18
 SQ SEQUENCE 18 AA; 1936 MW; D8FBFA226AA6DDDD9 CRC64;

Query Match 41.9%; Score 18; DB 6; Length 18;
 Best Local Similarity 50.0%; Pred. No. 3.6e+03;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 GSALFL 9
 | : ||:
 Db 7 GDVAFV 12

RESULT 23

Q9T2G8 PRELIMINARY; PRT; 18 AA.
 AC Q9T2G8;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE CARBONIC ANHYDRASE (EC 4.2.1.1) (FRAGMENT).
 OS Solanum tuberosum (potato).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; Asteridae; euasterids I; Solanales;
 OC Solanaceae; Solanum.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 96327808.
 RA Rumeau D., Guine S., Fina L., Gault N., Nicole M., Peltier G.;
 RT "Subcellular distribution of carbonic anhydrase in Solanum tuberosum
 L. leaves: characterization of two compartment-specific isoforms.";
 RL Planta 199;79-88(1996).
 SQ SEQUENCE 18 AA; 2017 MW; 5F515AD3CDD3292E CRC64;

Query Match 41.9%; Score 18; DB 8; Length 18;
 Best Local Similarity 80.0%; Pred. No. 3.6e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GSALF 8
 | : ||:
 Db 7 GSKAF 11

RESULT 24

Q9UMM9 PRELIMINARY; PRT; 19 AA.
 AC Q9UMM9;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE ARGININE VASOPRESSIN-NEUROPHYSIN II (FRAGMENT).
 GN AVP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 91123474.
 RA Ito M., Mori Y., Oiso Y., Saito H.;
 RT "A single base substitution in the coding region for neurophysin II
 RT associated with familial central diabetes insipidus."
 RL J. Clin. Invest. 87:725-728(1991).
 DR EMBL; M63733; AAA69844.1; -.
 FT NON_TER 19
 SQ SEQUENCE 19 AA; 1985 MW; 5FF5FCD7BD990451 CRC64;

Query Match 41.9%; Score 18; DB 4; Length 19;
 Best Local Similarity 80.0%; Pred. No. 3.8e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GSALF 8
 | : ||:
 Db 7 GSKAF 11

Db 12 GLLAF 16

RESULT 25

Q73129 PRELIMINARY; PRT; 19 AA.
 ID Q73129;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last annotation update)
 DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
 GN ENV.
 OS human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SAMPLE P4.25-15;
 RA Wolinsky S.M., Korber B.T.M., Neumann A.U., Daniels M., Kunstman K.J.,
 RA Whetseil A.J., Cao Y., Ho D.D., Safritz J.T., Koup R.A.;
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SAMPLE P4.25-15;
 RA McDonald D.;
 RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U36027; AAA97722.1; -.
 KW Envelope protein.
 FT NON_TER 1
 SQ SEQUENCE 19 AA; 2066 MW; E117102D52800EF4 CRC64;

Query Match 41.9%; Score 18; DB 12; Length 19;
 Best Local Similarity 100.0%; Pred. No. 3.8e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GSALF 7
 | : ||:
 Db 1 GSALF 4

Search completed: November 14, 2000, 11:57:48
 Job time: 55 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 14, 2000, 11:56:53 ; Search time 12.04 Seconds
(without alignments)
12.529 Million cell updates/sec

Title: us-09-277-074-10

Perfect score: 43

Sequence: 1 KIFGSLAFL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 164575 seqs, 16761186 residues

Total number of hits satisfying chosen parameters: 87906

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*

2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*

3: /cgn2_6/ptodata/2/iaa/6_COMB.pep.*

4: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*

5: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	100.0	9	1	US-08-467-083-27
2	43	100.0	9	1	US-08-787-547-70
3	43	100.0	9	1	US-08-414-417B-27
4	43	100.0	9	2	US-08-486-348A-27
5	43	100.0	9	2	US-08-468-545B-27
6	43	100.0	9	2	US-08-902-516-18
7	43	100.0	9	3	US-08-466-680B-27
8	43	100.0	9	4	PCT-US95-16415-10
9	43	100.0	16	1	US-08-467-083-62
10	43	100.0	16	1	US-08-414-417B-62
11	43	100.0	16	2	US-08-486-348A-62
12	43	100.0	16	2	US-08-468-545B-62
13	43	100.0	16	3	US-08-466-680B-62
14	29	67.4	15	1	US-08-467-083-36
15	29	67.4	15	1	US-08-414-417B-36
16	29	67.4	15	2	US-08-486-348A-36
17	29	67.4	15	2	US-08-468-545B-36
18	29	67.4	15	3	US-08-466-680B-36
19	24	55.8	9	1	US-08-215-805A-11
20	24	55.8	15	1	US-08-467-083-42
21	24	55.8	15	1	US-08-414-417B-42
22	24	55.8	15	2	US-08-486-348A-42
23	24	55.8	15	2	US-08-468-545B-42
24	24	55.8	15	3	US-08-466-680B-42
25	24	55.8	17	1	US-08-237-418-24
26	24	55.8	19	3	US-08-486-099-141
27	24	55.8	19	3	US-08-484-223B-141
28	24	55.8	19	3	US-08-919-597-141

29	24	55.8	19	3	US-08-475-668A-141	Sequence 141, App
30	24	55.8	19	3	US-08-485-551A-141	Sequence 141, App
31	24	55.8	19	3	US-08-471-913A-141	Sequence 141, App
32	23	53.5	11	1	US-08-799-825-15	Sequence 15, Appl
33	23	53.5	17	2	US-08-487-890A-104	Sequence 104, App
34	23	53.5	17	2	US-08-478-435-104	Sequence 104, App
35	23	53.5	17	2	US-08-337-483-104	Sequence 104, App
36	23	53.5	17	2	US-08-478-373-104	Sequence 104, App
37	23	53.5	17	3	US-08-474-671-104	Sequence 104, App
38	23	53.5	17	3	US-08-483-577A-104	Sequence 104, App
39	23	53.5	20	4	PCT-US95-12502-28	Sequence 28, Appl
40	22	51.2	10	3	US-08-467-580-115	Sequence 115, App
41	22	51.2	10	4	PCT-US95-08516-115	Sequence 115, App
42	22	51.2	11	2	US-08-799-825-20	Sequence 20, Appl
43	22	51.2	14	2	US-09-133-774-9	Sequence 9, Appl1
44	22	51.2	14	3	US-09-303-862-9	Sequence 9, Appl1
45	22	51.2	14	3	US-08-466-368-7	Sequence 7, Appl1

ALIGNMENTS

RESULT 1
US-08-467-083-27
; Sequence 27, Application US/08467083
; Patent No. 5726023
; GENERAL INFORMATION:
; APPLICANT: Cheever, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,083
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/414,417
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; TELEX: 3723836 SEEDANBERRY
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-467-083-27

Query Match 100.0%; Score 43; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIFGSLAFL 9
Db 1 KIFGSLAFL 9

RESULT 2

US-08-787-547-70
; Sequence 70, Application US/08787547
; Patent No. 5783567
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Cufley, Joanne M.
; APPLICANT: Langer, Robert S.
; TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY
; TITLE OF INVENTION: OF NUCLEIC ACID
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/787,547
; FILING DATE: 22-JAN-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/003001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-787-547-70

Query Match 100.0%; Score 43; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIFGSLAFL 9
Db 1 KIFGSLAFL 9

RESULT 3

US-08-414-417B-27
; Sequence 27, Application US/08414417B
; Patent No. 5801005
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,417B
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-414-417B-27

Query Match 100.0%; Score 43; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIFGSLAFL 9
Db 1 KIFGSLAFL 9

RESULT 4

US-08-486-348A-27
; Sequence 27, Application US/08486348A
; Patent No. 5846538
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,348A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900

Query Match 100.0%; Score 43; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIFGSLAFL 9
Db 1 KIFGSLAFL 9

RESULT 3

US-08-414-417B-27
; Sequence 27, Application US/08414417B
; Patent No. 5801005
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:

TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 27:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 US-08-466-348A-27

Query Match 100.0%; Score 43; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIFGSLAFL 9
 |||||
 DB 1 KIFGSLAFL 9

RESULT 5

US-08-468-545B-27
 Sequence 27, Application US/08468545B
 Patent No. 5876712

GENERAL INFORMATION:
 APPLICANT: Cheever, Martin A.
 APPLICANT: Disis, Mary L.
 TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
 TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
 TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
 NUMBER OF SEQUENCES: 69
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Seed and Berry LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: US
 ZIP: 98104-7092

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/468,545B
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
 NAME: Sharkey, Richard G.
 REGISTRATION NUMBER: 32,629
 REFERENCE/DOCKET NUMBER: 920010.448C5

TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear

US-08-468-545B-27

Query Match 100.0%; Score 43; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIFGSLAFL 9
 |||||
 DB 1 KIFGSLAFL 9

RESULT 6

US-08-902-516-18

Sequence 18, Application US/08902516
 Patent No. 5891432

GENERAL INFORMATION:
 APPLICANT: SOO HOO, William
 TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS
 TITLE OF INVENTION: COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE
 TITLE OF INVENTION: RESPONSE USING SAME
 NUMBER OF SEQUENCES: 50
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CAMPBELL & FLORES, LLP
 STREET: 4370 La Jolla Village Drive, Suite 700
 CITY: San Diego
 STATE: California
 COUNTRY: United States
 ZIP: 92121

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/902,516
 FILING DATE: 29-JUL-1997
 CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Cathryn A.
 REGISTRATION NUMBER: 31,815
 REFERENCE/DOCKET NUMBER: P-IM 2442

TELEPHONE: (619)535-9001
 TELEFAX: (619)535-8949
 INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

US-08-902-516-18

Query Match 100.0%; Score 43; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIFGSLAFL 9
 |||||
 DB 1 KIFGSLAFL 9

RESULT 7

US-08-466-680B-27

Sequence 27, Application US/08466680B
 Patent No. 6075122

GENERAL INFORMATION:
 APPLICANT: Cheever, Martin A.
 APPLICANT: Disis, Mary L.
 TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
 TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
 TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
 NUMBER OF SEQUENCES: 69
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Seed and Berry LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: US
 ZIP: 98104-7092

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/466,680B
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
 NAME: Sharkey, Richard G.
 REGISTRATION NUMBER: 32,629
 REFERENCE/DOCKET NUMBER: 920010.448C5

TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear

US-08-466-680B-27

Query Match 100.0%; Score 43; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIFGSLAFL 9
 |||||
 DB 1 KIFGSLAFL 9

RESULT 8

US-08-902-516-18

APPLICATION NUMBER: US/08/466,680B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C4
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-466-680B-27

Query Match 100.0%; Score 43; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIFGSLAFL 9
| | | | | | | | | |
DB 1 KIFGSLAFL 9

RESULT 8
PCT-US95-16415-10
Sequence 10, Application PC/TUS9516415
GENERAL INFORMATION:
APPLICANT: The Scripps Research Institute
TITLE OF INVENTION: IN VIVO ACTIVATION OF TUMOR-SPECIFIC
TITLE OF INVENTION: CYTOTOXIC T CELLS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute
STREET: 10666 North Torrey Pines Road, TPC-8
CITY: La Jolla
STATE: California
COUNTRY: US
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16415
FILING DATE: 13-DEC-1995

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/355,558
FILING DATE: 14-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Logan, April C.
REGISTRATION NUMBER: 33,950
REFERENCE/DOCKET NUMBER: 433.1PC
TELEPHONE: (619) 554-2937
TELEFAX: (619) 554-6312
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US95-16415-10

Query Match 100.0%; Score 43; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KIFGSLAFL 9
| | | | | | | | | |
DB 1 KIFGSLAFL 9
RESULT 9
US-08-467-083-62
Sequence 62, Application US/08467083
Patent No. 5726023
GENERAL INFORMATION:
APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,083
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/414,417
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C2
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
TELEX: 3723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-467-083-62

Query Match 100.0%; Score 43; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIFGSLAFL 9
| | | | | | | | | |
DB 1 KIFGSLAFL 9

RESULT 10
US-08-414-417B-62
Sequence 62, Application US/08414417B
Patent No. 5801005
GENERAL INFORMATION:
APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED

```
;
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,417B
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-414-417B-62

Query Match 100.0%; Score 43; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIFGSLAFL 9
Db 1 KIFGSLAFL 9

RESULT 11
US-08-486-348A-62
; Sequence 62, Application US/08486348A
; Patent No. 5846538
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,348A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C6
```

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;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-486-348A-62

Query Match 100.0%; Score 43; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIFGSLAFL 9
Db 1 KIFGSLAFL 9

RESULT 12
US-08-468-545B-62
; Sequence 62, Application US/08468545B
; Patent No. 5876712
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,545B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-468-545B-62

Query Match 100.0%; Score 43; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIFGSLAFL 9
Db 1 KIFGSLAFL 9
```

RESULT 13
US-08-466-680B-62
; Sequence 62, Application US/0846680B
; Patent No. 6075122
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,680B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C4
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-466-680B-62

Query Match 100.0%; Score 43; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIFGSLAFL 9
| | | | | | | | | |
DB 1 KIFGSLAFL 9

RESULT 14
US-08-467-083-36
; Sequence 36, Application US/08467083
; Patent No. 5726023
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,083
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/414,417
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C2
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; TELEX: 3723836 SEEDANBERRY
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-467-083-36

Query Match 67.4%; Score 29; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIFGSL 6
| | | | | | | |
DB 10 KIFGSL 15

RESULT 15
US-08-414-417B-36
; Sequence 36, Application US/08414417B
; Patent No. 5801005
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,417B
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C2
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

US-08-414-417B-36

```

Query Match          67.4%; Score 29; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIFGSL 6
Db 10 KIFGSL 15

RESULT 16
US-08-486-348A-36
; Sequence 36, Application US/08486348A
; Patent No. 5846538
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disls, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,348A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 36:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-486-348A-36

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```

Query Match          67.4%; Score 29; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIFGSL 6
Db 10 KIFGSL 15

RESULT 17
US-08-468-545B-36
; Sequence 36, Application US/08468545B
; Patent No. 5876712
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disls, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED

```

```

; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,545B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-468-545B-36

Query Match          67.4%; Score 29; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIFGSL 6
Db 10 KIFGSL 15

RESULT 18
US-08-466-680B-36
; Sequence 36, Application US/08466680B
; Patent No. 6075122
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disls, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,680B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C4
; TELECOMMUNICATION INFORMATION:

```

TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-466-680B-36

Query Match 67.4%; Score 29; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIFGSL 6
 |||||
DB 10 KIFGSL 15

RESULT 19

US-08-215-805A-11
Sequence 11, Application US/08215805A
Patent No. 5559008
GENERAL INFORMATION:
APPLICANT: Chang, Yung-Fu
TITLE OF INVENTION: LEUKOTOXIN GENE FROM PASTEURILLA
TITLE OF INVENTION: SUIS
NUMBER OF SEQUENCES: 84
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14603

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/215,805A
FILING DATE: 22-MAR-1994
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Timian, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 19603/61 (D-1329A)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1636
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Actinobacillus pleuropneumoniae
US-08-215-805A-11

Query Match 55.8%; Score 24; DB 1; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.2e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 FGSLAF 8
 ||||
DB 2 FGSKAF 7

RESULT 20

US-08-467-083-42
Sequence 42, Application US/08467083
Patent No. 5726023
GENERAL INFORMATION:
APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,083
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/414,417
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-467-083-42

Query Match 55.8%; Score 24; DB 1; Length 15;
Best Local Similarity 62.5%; Pred. No. 54;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KIFGSLAF 8
 |: || |
DB 2 KVLGSGAF 9

RESULT 21

US-08-414-417B-42
Sequence 42, Application US/08414417B
Patent No. 5801005
GENERAL INFORMATION:
APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.

TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/414,417
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-467-083-42

; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/414,417B
 ; FILING DATE: 31-MAR-1995
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Sharkey, Richard G.
 ; REGISTRATION NUMBER: 32,629
 ; REFERENCE/DOCKET NUMBER: 920010.448C2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 622-4900
 ; TELEFAX: (206) 682-6031
 ; INFORMATION FOR SEQ ID NO: 42:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 15 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; US-08-414-417B-42

Query Match 55.8%; Score 24; DB 1; Length 15;
 Best Local Similarity 62.5%; Pred. No. 54;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KIFGSLAF 8
 I: | | | |
 Db 2 KVLGSGAF 9

RESULT 22
 US-08-486-348A-42
 ; Sequence 42, Application US/08486348A
 ; Patent No. 5846538
 ; GENERAL INFORMATION:
 ; APPLICANT: Cheever, Martin A.
 ; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
 ; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
 ; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
 ; NUMBER OF SEQUENCES: 69
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Seed and Berry LLP
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue
 ; CITY: Seattle
 ; STATE: Washington
 ; COUNTRY: US
 ; ZIP: 98104-7092
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/486,348A
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Sharkey, Richard G.
 ; REGISTRATION NUMBER: 32,629
 ; REFERENCE/DOCKET NUMBER: 920010.448C6
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 622-4900
 ; TELEFAX: (206) 682-6031
 ; INFORMATION FOR SEQ ID NO: 42:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 15 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; US-08-486-348A-42

Query Match 55.8%; Score 24; DB 2; Length 15;
 Best Local Similarity 62.5%; Pred. No. 54;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KIFGSLAF 8
 I: | | | |
 Db 2 KVLGSGAF 9

RESULT 23
 US-08-468-545B-42
 ; Sequence 42, Application US/08468545B
 ; Patent No. 5876712
 ; GENERAL INFORMATION:
 ; APPLICANT: Cheever, Martin A.
 ; APPLICANT: Disis, Mary L.
 ; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
 ; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
 ; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
 ; NUMBER OF SEQUENCES: 69
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Seed and Berry LLP
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue
 ; CITY: Seattle
 ; STATE: Washington
 ; COUNTRY: US
 ; ZIP: 98104-7092
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/468,545B
 ; FILING DATE: 06-JUN-1995
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Sharkey, Richard G.
 ; REGISTRATION NUMBER: 32,629
 ; REFERENCE/DOCKET NUMBER: 920010.448C5
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 622-4900
 ; TELEFAX: (206) 682-6031
 ; INFORMATION FOR SEQ ID NO: 42:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 15 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; US-08-468-545B-42

Query Match 55.8%; Score 24; DB 2; Length 15;
 Best Local Similarity 62.5%; Pred. No. 54;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KIFGSLAF 8
 I: | | | |
 Db 2 KVLGSGAF 9

RESULT 24
 US-08-466-680B-42
 ; Sequence 42, Application US/08466680B
 ; Patent No. 6075122
 ; GENERAL INFORMATION:
 ; APPLICANT: Cheever, Martin A.
 ; APPLICANT: Disis, Mary L.
 ; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
 ; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
 ; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
 ; NUMBER OF SEQUENCES: 69
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Seed and Berry LLP
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue
 ; CITY: Seattle
 ; STATE: Washington
 ; COUNTRY: US
 ; ZIP: 98104-7092
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/466,680B
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Sharkey, Richard G.
 ; REGISTRATION NUMBER: 32,629
 ; REFERENCE/DOCKET NUMBER: 920010.448C6
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 622-4900
 ; TELEFAX: (206) 682-6031
 ; INFORMATION FOR SEQ ID NO: 42:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 15 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; US-08-466-680B-42

ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,680B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-466-680B-42

Query Match 55.8%; Score 24; DB 3; Length 15;
Best Local Similarity 52.5%; Pred. No. 54;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KIFGSLAF 8
Db 2 KVLGSGAF 9

RESULT 25

US-08-237-418-24
Sequence 24, Application US/08237418
Patent No. 5601973
GENERAL INFORMATION:
APPLICANT: Mueller, Martin
APPLICANT: Glissmann, Lutz
TITLE OF INVENTION: Seroreactive Regions on HPV 16 Proteins
TITLE OF INVENTION: E1 and E2
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/237,418
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/913,613
FILING DATE: 16-JUL-1992
APPLICATION NUMBER: DE P 41 23 760.9
FILING DATE: 18-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Einaudi, Carol P.

REGISTRATION NUMBER: 33,220
REFERENCE/DOCKET NUMBER: 02481-1199-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-237-418-24

Query Match 55.8%; Score 24; DB 1; Length 17;
Best Local Similarity 80.0%; Pred. No. 61;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIFGS 5
Db 7 KVFSG 11

Search completed: November 14, 2000, 11:58:19
Job time: 86 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 14, 2000, 11:56:53 ; Search time 14.72 Seconds
(without alignments)
20.907 Million cell updates/sec

Title: US-09-277-074-10

Perfect score: 43

Sequence: 1 KIFGSLAFL 9

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 127583

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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19: /SIDSL/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SIDSL/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SIDSL/gcgdata/geneseq/geneseq/AA2000.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	100.0	9	15	Antigen fragment 1
2	43	100.0	9	17	Cytotoxic T lympho
3	43	100.0	9	18	Immunogenic peptid
4	43	100.0	9	19	HER-2/neu syntheti
5	43	100.0	9	19	HER-1/neu protein
6	43	100.0	9	19	HER-2/neu derived
7	43	100.0	9	20	HLA Class I motif
8	43	100.0	15	21	HLA class II bindi
9	29	67.4	17	21	Human gene 16-enco
10	25	58.1	7	20	Membrane dipeptida
11	25	58.1	16	21	Amino acid sequenc
12	25	58.1	16	21	Amino acid sequenc

13	25	58.1	18	20	W95382	Antimicrobial pept
14	24	55.8	7	19	W60420	Tumour homing pept
15	24	55.8	7	20	W93747	Mouse B16B15b mela
16	24	55.8	11	20	W93317	r-CGRP-alpha-27-37
17	24	55.8	15	21	Y98857	HLA class II bindi
18	24	55.8	16	16	R64603	RF-1 peptide 48 fr
19	24	55.8	17	16	R64604	RF-1 peptide 49 fr
20	24	55.8	18	4	P30110	Sequence of Vp1 ca
21	24	55.8	18	16	R64605	RF-1 peptide 50 fr
22	24	55.8	19	16	R64606	RF-1 peptide 51 fr
23	24	55.8	19	21	Y89178	Core polypeptide f
24	24	55.8	20	16	R64607	RF-1 peptide 52 fr
25	23	53.5	9	21	Y82864	Uroplakin tumour a
26	23	53.5	13	15	R47159	Sequence of Trypsin
27	23	53.5	13	15	R55383	Human LDL receptor
28	23	53.5	15	8	P70720	Equine influenza v
29	23	53.5	17	21	Y51778	H. Influenzae type
30	23	53.5	17	21	Y80371	H. Influenzae tran
31	23	53.5	20	17	R98037	Fusogenic peptide
32	22	51.2	10	17	R92635	VLA-4 binding pept
33	22	51.2	14	20	Y42730	Chlamydia trachoma
34	22	51.2	14	20	W84057	Human V3 loop HIV
35	22	51.2	14	21	Y83819	Chlamydia trachoma
36	22	51.2	15	19	W62154	Agrobacterium faec
37	22	51.2	15	21	Y98943	HLA class II bindi
38	22	51.2	16	18	W32320	Leishmania immunog
39	22	51.2	17	21	Y44796	C1-protein with mu
40	22	51.2	18	20	Y41953	Rheumatoid arthrit
41	22	51.2	18	20	Y02863	Fragment of human
42	22	51.2	20	15	R60722	Lolium perenne pro
43	22	51.2	20	15	R60723	Lolium perenne pro
44	22	51.2	20	15	R60724	Lolium perenne pro
45	22	51.2	20	15	R60725	Lolium perenne pro

ALIGNMENTS

RESULT 1
R73685
ID R73685 standard; peptide; 9 AA.
XX
AC R73685;
XX
DT 14-JUN-1995 (first entry)
XX
DE Antigen fragment 1, from c-ERB2 has binding affinity for HLA-2.1.
XX
KW antigen; epitope; immunogenic target protein; PSA; HBVc; HBVs; EBV;
KW HIV1; plasma specific antigen; hepatitis B virus; Epstein Barr;
KW human immunodeficiency virus; human papilloma virus; p53; c-ERB2;
KW MAGE-1; melanoma antigen-1; core antigen; surface antigen;
KW pharmaceutical composition; in vivo; ex vivo; therapeutic;
KW diagnostic; MIC class I molecule; major histocompatibility complex;
KW HLA-A2.1; 9mer; 10mer; anchor; human leukocyte antigen; PLP; 8mer;
KW algorithm prediction; MBP; CMV; cytomegalovirus; HSV;
KW herpes simplex virus.
XX
OS Homo sapiens.
XX
FN W09420127-A.
XX
PD 15-SEP-1994.
XX
PF 04-MAR-1994; 94WO-US02353.
XX
PR 05-MAR-1993; 93US-0027146.
PR 04-JUN-1993; 93US-0073205.
PR 29-NOV-1993; 93US-0159184.
XX
PA (CYTE-) CYTEL CORP.
XX
PI Grey HM, Kast WM, Sette A, Sidney J;

XX WPI; 1994-302678/37.
 XX
 XX Immunogenic peptide(s) having an HLA-A2.1 binding motif - used
 PT for treatment or prophylaxis of cancer, virus infection or
 PT autoimmune diseases.
 XX
 XX Disclosure; Page 80; 138pp; English.
 XX
 XX R73685-876 are potential peptide binders of HLA-A2.1 motif. Using
 CC motifs disclosed in the invention, these peptides were screened for
 CC further motifs. Only peptides with binding affinity of at least 1%
 CC (binding affinity is expressed as an IC50 value) as compared to the
 CC standard peptide (R71293) in assays. This peptide has a binding
 CC value of 0.1500. The peptides of the invention can induce cytotoxic
 CC T lymphocytes which can react with target cells. They can be used for
 CC the treatment or prophylaxis of cancer, eg. prostate cancer or
 CC lymphoma, etc.
 XX
 XX Sequence 9 AA;
 SQ

Query Match 100.0%; Score 43; DB 15; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIFGSLAFL 9
 DB 1 kifgslaf1 9
 |||||

RESULT 2
 R97507
 ID R97507 standard; peptide; 9 AA.
 XX
 AC R97507;
 XX
 DT 11-FEB-1997 (first entry)
 XX
 DE Cytotoxic T lymphocyte-activating Her-2/Neu-specific peptide.
 XX
 KW p53; Her-2; Neu; aa; amino acid; CTL; cytotoxic T lymphocyte; target;
 KW malignant cell; antigenic; vaccine; immunisation; activation.
 XX
 OS Homo sapiens.
 XX
 PN W09618409-A1.
 XX
 PD 20-JUN-1996.
 XX
 PF 14-DEC-1995; 95WO-US16415.
 XX
 PR 14-DEC-1994; 94US-0355558.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Sherman LA;
 XX
 DR WPI; 1996-300385/30.
 XX
 XX In vivo activation of tumour-specific cytotoxic T lymphocytes - by
 PT contacting with polypeptide(s) derived from human p53 or Her-2/Neu
 PT proteins
 PT
 XX
 XX Claim 5; Page 124; 158pp; English.
 PS
 XX R97507 is a peptide capable of activating cytotoxic T lymphocytes
 CC (CTLs) which specifically target malignant cells. The peptide
 CC corresponds to amino acids 369-377 of human Her-2/Neu protein. CTL-
 CC activating peptides can be used in a vaccine for protecting against
 CC tumour cell formation. CTLs activated by the peptides will lyse
 CC tumour cells displaying specific peptides. Antibodies against CTL-
 CC activating peptides are useful for the identification of other

CC similar compounds which may be useful for treating cancer or virally-
 CC infected cells, or for diagnosis. The peptide and vaccines produced
 CC provide immunity to a high percentage of different ethnic groups,
 CC i.e. those with different HLA alleles.
 XX
 XX Sequence 9 AA;
 SQ

Query Match 100.0%; Score 43; DB 17; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIFGSLAFL 9
 DB 1 kifgslaf1 9
 |||||

RESULT 3
 W36824
 ID W36824 standard; peptide; 9 AA.
 XX
 AC W36824;
 XX
 DT 23-MAR-1998 (first entry)
 XX
 DE Immunogenic peptide H3 based on the human Her-2/neu protein.
 XX
 KW Her-2/neu protein; human leukocyte antigen A2.1; HLA;
 KW cytotoxic T lymphocyte; CTL; immune response; tumour-associated antigen;
 KW T-cell receptor; TCR; tumour treatment.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN W09732603-A1.
 XX
 PD 12-SEP-1997.
 XX
 PF 05-MAR-1997; 97WO-US03611.
 XX
 PR 05-MAR-1996; 96US-0012845.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Lustgarten J, Sherman LA;
 XX
 DR WPI; 1997-470496/43.
 XX
 PT Nucleic acid encoding variable regions of HLA-restricted non-human T
 PT cell receptor specific for tumour antigen - used to identify tumour
 PT antigens and for tumour therapy
 XX
 XX Example 1; Page 9; 34pp; English.
 PS
 XX Synthetic peptides W36824-40 are based on the sequence of the human
 CC Her-2/neu protein, wherein each sequence contains the anchor motif
 CC human leukocyte antigen (HLA) A2.1. The present peptide is based on
 CC positions 369-377. The ability of these peptides to inhibit the binding
 CC of an influenza virus matrix protein peptide M1 to HLA A2.1 was measured
 CC by inhibition of lysis by an M1 specific, HLA A2.1 restricted, cytotoxic
 CC T lymphocyte (CTL) clone. The present protein showed 38% inhibition. The
 CC peptides were also tested for their ability to elicit an immune response
 CC in vivo. However, only H3 (W36824) and H7 (W36826) were able to do
 CC this. H3 and H7 peptides are tumour-associated antigens, and were used to
 CC immunize a transgenic, non-human vertebrate (that has been modified to
 CC express at least one HLA antigen), so that the animal produces CTL which
 CC displays HLA-restricted T-cell receptor (TCR) specificity for the
 CC antigen. Nucleic acid encoding variable regions of the alpha and beta
 CC chains of such TCRs can be amplified from CTLs produced in the above
 CC manner. Cells expressing recombinant TCR are used to identify antigens
 CC associated with a tumour and to treat tumours in humans. Transgenic mice
 CC are a more convenient source of CTL than the tumour-infiltrating
 CC lymphocytes previously used. TCR can be humanised to reduce

CC side-reactions and short peptide derivatives of TCR are more economical
 CC to produce than TCR itself, particularly when expressed as a
 CC single-chain molecule rather than as a dimer.
 XX
 XX Sequence 9 AA;

Query Match 100.0%; Score 43; DB 18; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIFGSLAFL 9
 |||||
 Db 1 kifgslaf1 9

RESULT 4
 W71131
 ID W71131 standard; peptide; 9 AA.
 XX
 AC W71131;
 XX
 DT 16-NOV-1998 (first entry)
 XX
 DE HER-2/neu synthetic peptide epitope 1.
 XX
 KW Tyrosinase; tyrosinase cytotoxic lymphocyte response;
 KW cytotoxic T lymphocyte; cysteine-depleted; melanoma.
 XX
 OS Synthetic.
 XX
 PN WO9833810-A2.
 XX
 PD 06-AUG-1998.
 XX
 PF 29-JAN-1998; 98WO-US01592.
 XX
 PR 30-JAN-1997; 97US-0037781.
 XX
 PA (UVVI-) UNIV VIRGINIA PATENT FOUND.
 XX
 PI Engelhard VH, Hunt DF, Kittlesen D, Slingluff CL;
 XX
 DR WPI; 1998-437388/37.
 XX
 CC Disease specific immunogen - comprises disease specific cytotoxic T
 CC lymphocyte epitope used to elicit melanoma specific CTL response
 CC
 PS Disclosure; Page 27; 93pp; English.
 XX
 CC The peptide epitope W7119-W7118 were created for human tumour-specific
 CC cytotoxic T lymphocyte response. These peptides are cysteine-
 CC depleted mutants of a native disease-specific CTL epitope. The cysteine-
 CC depleted CTL epitopes elicit a stronger or more specific CTL response
 CC than the native epitope. The epitopes can be used in a disease-specific
 CC immunogen to protect a mammal against disease in particular melanomas.
 CC The peptides may also be used to screen a sample for the presence of
 CC an antigen with the same epitope, or with a different cross-reactive
 CC epitope.
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 43; DB 19; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIFGSLAFL 9
 |||||
 Db 1 kifgslaf1 9

RESULT 5

W78859
 ID W78859 standard; peptide; 9 AA.
 XX
 AC W78859;
 XX
 DT 17-NOV-1998 (first entry)
 XX
 DE HER-1/neu protein fragment 369-377.
 XX
 KW Microparticle; delivery; polymeric matrix; autoantigen; tumour antigen;
 KW class II associated peptide; pathogen; gene therapy; genetic disease;
 KW infection; downregulation; immune response.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO9831398-A1.
 XX
 PD 23-JUL-1998.
 XX
 PF 22-JAN-1998; 98WO-US01499.
 XX
 PR 06-JAN-1998; 98US-0003253.
 PR 22-JAN-1997; 97US-0787547.
 XX
 PA (PANG-) PANGAEA PHARM INC.
 XX
 PI Curley JM, Hedley ML, Langer RS, Lunsford LB;
 XX
 DR WPI; 1998-427556/36.
 XX
 CC New preparations of microparticles - comprising a synthetic polymer
 CC matrix and nucleic acid comprising an expression vector for use in
 CC gene therapy
 CC
 PS Disclosure; Page 10; 101pp; English.
 XX
 CC A microparticle preparation (MP) has been developed, consisting of
 CC microparticles having a diameter of less than 100 mu m. The MP comprises:
 CC (a) a polymeric matrix (PM) consisting of one or more synthetic polymers
 CC having a solubility in water of less than 1 mg/l; and (b) an expression
 CC vector selected from RNA molecules (at least 50% of which are closed
 CC circles) or circular plasmid DNA (at least 50% of which are supercoiled).
 CC Also described is a MP of at most 20 microns in diameter, comprising: (a)
 CC a PM; and (b) a NAM comprising an expression control sequence operatively
 CC linked to a coding sequence, where the coding sequence encodes an
 CC expression product selected from: (i) a polypeptide at least 7 amino
 CC acids in length, having a sequence identical to the sequence of: (1) a
 CC fragment of a naturally-occurring mammalian protein; or (ii) a fragment
 CC of a naturally-occurring protein from an infectious agent which infects
 CC a mammal; (2) a peptide having a length and sequence which permits it to
 CC bind to an MHC class I or II molecule; and (3) the polypeptide or the
 CC peptide linked to a trafficking sequence. W69763 to W69765, and W78793
 CC to W78897 are peptide fragments for use in the present invention. The
 CC MPs are highly effective vehicles for the delivery of polynucleotides
 CC into phagocytic cells. They can be used for gene therapy, e.g. for
 CC treating genetic diseases, infections or tumours or for downregulating
 CC an immune response.
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 43; DB 19; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIFGSLAFL 9
 |||||
 Db 1 kifgslaf1 9

RESULT 6
 W70057

ID XX W70057 standard; peptide; 9 AA.
 AC XX W70057;
 XX XX
 DT XX 22-OCT-1998 (first entry)
 XX XX
 DE XX HER-2/neu derived HLA-A2.1 binding peptide 5 (residues 369-377).
 XX XX
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW human leukocyte antigen; HLA; tumour associated antigen; cancer;
 KW antigen presenting cell; APC; immunogenic peptide; immune disorder;
 KW viral infection; AIDS; hepatitis; bacterial infection; malaria;
 KW fungal infection; tuberculosis; melanoma; HER-2/neu; cerB-2.
 XX XX
 OS Synthetic.
 OS Homo sapiens.
 XX XX
 PN WO9833888-AL.
 XX XX
 PD 06-AUG-1998.
 XX XX
 XX 30-JAN-1998; 98WO-US01959.
 XX XX
 PR 31-JAN-1997; 97US-0036696.
 XX XX
 PA (EPIM-) EPIMMUNE INC.
 XX XX
 PI Cells E, Sette A, Sidney J, Southwood S, Tsai V;
 XX XX
 DR WPI; 1998-437445/37.
 XX XX
 XX Production of antigen-specific cytotoxic T cells - by incubating
 PT immunogenic peptide(s) from antigen that binds class I major
 PT histocompatibility complex molecules with pre-treated antigen
 PT presenting cells
 XX XX
 PS Example 7; Page 77; 104pp; English.
 XX XX
 CC Sequences shown in W70053 to W70075 represent peptides derived from
 CC HER-2/neu (cerB-2) antigen. The peptides can bind to a human leukocyte
 CC antigen (HLA). HLA-A2.1 and are used to exemplify the method of
 CC invention of producing antigen-specific cytotoxic T cells (CTLs) in
 CC vitro. The method comprises contacting immunogenic peptides from an
 CC antigen that binds class I major histocompatibility complex (MHC)
 CC molecules with antigen presenting cells (APCs) pretreated with
 CC pretreatment growth factors, and incubating the APCs with purified CD8
 CC cells in the presence of at least 2 incubation growth factors, thereby
 CC producing antigen-specific CTLs. A method for specifically killing
 CC target cells in a human patient is also provided which comprises
 CC obtaining a fluid sample containing CTLs from a patient, contacting the
 CC cytotoxic T cells with APCs pretreated with pre-treatment growth factors,
 CC where the APCs comprise class I MHC molecules. The pretreated APCs are
 CC incubated with the cytotoxic growth factors, thereby producing activated
 CC CTLs which are contacted with a carrier to form a composition. The
 CC composition can then be administered to the patient. The activated CTLs
 CC can be used for treating cancers, immune disorders, viral infections,
 CC AIDS, hepatitis, bacterial infection, fungal infection, malaria or
 CC tuberculosis.
 XX XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 43; DB 19; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KIFGSLAFL 9
 |||||
 Db 1 kifgslaf1 9

RESULT 7
 Y10495

ID XX Y10495 standard; Peptide; 9 AA.
 AC XX Y10495;
 XX XX
 DT XX 12-MAY-1999 (first entry)
 XX XX
 DE XX HLA Class I motif peptide SEQ ID NO:425.
 XX XX
 KW Cytotoxic T-lymphocyte response; CTL; antigen; lymphatic system;
 KW immunisation; tumour; infectious disease; immunotherapy; cancer;
 KW malignant melanoma; viral disease; hepatitis; AIDS.
 XX XX
 OS Synthetic.
 OS Homo sapiens.
 XX XX
 PN WO9902183-A2.
 XX XX
 PD 21-JAN-1999.
 XX XX
 XX 10-JUL-1998; 98WO-US14289.
 XX XX
 PR 10-DEC-1997; 97US-0988320.
 PR 10-JUL-1997; 97CA-2209815.
 XX XX
 PA (CTLI-) CTL IMMUNOTHERAPIES CORP.
 XX XX
 PI Kuendig TM, Simard JLL;
 XX XX
 DR WPI; 1999-120514/10.
 XX XX
 XX Inducing a cytotoxic T lymphocyte response - by maintaining a level
 PT of antigen in the lymphatic system of a mammal so as to provide a
 PT sustained CTL response, used to treat, e.g. AIDS
 XX XX
 PS Disclosure; Page 43; 199pp; English.
 XX XX
 CC The present invention describes a method of inducing and/or sustaining
 CC an immunological cytotoxic T lymphocyte (CTL) response in a mammal. The
 CC method comprises: (a) delivering an antigen to the mammal at a level to
 CC induce an immunological CTL response in the mammal; and (b) maintaining
 CC the level of the antigen in the mammal's lymphatic system to maintain
 CC the immunologic CTL response. The method can be used for the delivery of
 CC e.g. a differentiation antigen, a tumour-specific multineage antigen,
 CC an embryonic antigen, an oncogene antigen, a mutated tumour-suppressor
 CC gene antigen, or a viral antigen. They can be used for the treatment of
 CC disease such as cancer, e.g. malignant melanoma or infectious disease,
 CC e.g. viral disease such as hepatitis or AIDS. Sustained antigen delivery
 CC to the lymphatic system provides for potent CTL stimulation that takes
 CC place in the milieu of the lymphoid organ, and it sustains stimulation
 CC that is necessary to keep CTL active, cytotoxic and recirculating
 CC through the body. Y10071 to Y10639 represent examples of peptide
 CC antigens given in the present invention.
 XX XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 43; DB 20; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KIFGSLAFL 9
 |||||
 Db 1 kifgslaf1 9

RESULT 8
 Y98846
 ID Y98846 standard; Peptide; 15 AA.
 XX XX
 AC Y98846;
 XX XX
 XX 07-AUG-2000 (first entry)
 XX XX

DE HLA class II binding antigen epitope peptide #35.

KW Human leucocyte antigen: HLA class II; antigen epitope; pharmaceutical;

KW immune response; chronic viral disease; cancer; autoimmune disease;

KW rheumatoid arthritis; multiple sclerosis; myasthenia gravis; AIDS;

KW allograft rejection; allergy; Lyme disease; hepatitis; prostate cancer;

KW glomerulonephritis; food hypersensitivity; malaria.

XX Unidentified.

OS WO9961916-A1.

PN 02-DEC-1999.

XX 28-MAY-1999; 99WO-US12066.

PF 29-MAY-1998; 98US-0087192.

XX (EPIM-) EPIMUNE INC.

XX Sette A, Southwood S, Sidney J;

PI WPI; 2000-097143/08.

XX New compositions containing immunogenic peptide epitopes for various

PT HLA class II DR molecules useful for inducing helper T cell response

PS Claim 1; Page 40; 60pp; English.

XX The present invention relates to a new pharmaceutical composition

CC comprising a unit dose form of a peptide, or analogue, comprising an

CC epitope selected from those represented by peptides Y9812-Y9939 which

CC are derived from various antigens for various human leucocyte antigen

CC class DR molecules, representative of the world wide population. The

CC peptide/analogue binds to an HLA class II molecule at an IC-50 of less

CC than or equal to 1,000 nM. The pharmaceutical can be used to induce a

CC helper T cell response. The pharmaceutical focuses the immune response

CC towards selected determinants and could therefore be used in cases of

CC chronic viral diseases and cancer. Examples of diseases that can be

CC treated using the peptide containing pharmaceutical include autoimmune

CC diseases (rheumatoid arthritis, multiple sclerosis, and myasthenia

CC gravis), allograft rejection, allergies, Lyme disease, hepatitis,

CC post-streptococcal endocarditis or glomerulonephritis and food

CC hypersensitivities. The peptide epitopes can be used to enhance immune

CC responses against other immunogens administered with the peptides.

CC Diseases which can be treated using immunogenic mixtures include prostate

CC cancer, hepatitis B, hepatitis C, AIDS, renal carcinoma, cervical

CC carcinoma, lymphoma, and condyloma acuminatum. The peptides may also be

CC used to make monoclonal antibodies useful as potential diagnostic or

CC therapeutic agents. The peptides may also be useful as diagnostic

CC reagents, for example, to determine the susceptibility of an individual

CC to a treatment regimen. Also, the peptides may be used to predict which

CC individuals will be at substantial risk of developing chronic infection.

CC The selection of appropriate T and B cell epitopes should allow the

CC development of epitope based vaccines particularly towards conserved

CC epitopes of pathogens which are characterized by high sequence

CC variability such as HIV, HCV and Malaria.

XX SQ Sequence 15 AA:

Query Match 100.0%; Score 43; DB 21; Length 15;

Best Local Similarity 100.0%; Pred. NO. 0.009;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIFGSLAFL 9

Db 3 kifgslaf1 11

RESULT 9

Y86381

ID Y86381 standard; peptide: 17 AA.

XX Y86381;

AC 19-APR-2000 (first entry)

DT Human gene 16-encoded protein fragment, SEQ ID NO:296.

XX

DE Human; secreted protein; cancer; tumour; developmental abnormality;

XX foetal deficiency; blood disorder; immune system disorder; inflammation;

KW autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;

KW schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;

KW atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;

KW digestive disorder; endocrine disorder; infection; AIDS; leukaemia;

KW therapy.

XX Homo sapiens.

OS WO9966041-A1.

XX 23-DEC-1999.

PN 15-JUN-1999; 99WO-US13418.

PD 16-JUN-1998; 98US-0089507.

PF 16-JUN-1998; 98US-0089508.

XX 16-JUN-1998; 98US-0089509.

PR 16-JUN-1998; 98US-0089510.

XX 22-JUN-1998; 98US-0090112.

XX 22-JUN-1998; 98US-0090113.

XX (HUMA-) HUMAN GENOME SCI INC.

PA Ruben SM, NI J, Rosen CA, Wel Y, Young PE, Florence KA;

XX Soppet DR, Brewer LA, Endress GA, Carter KC, Mucenski M, Ebner R;

PI Lafleur DW, Olsen HS, Shi Y, Moore PA, Komatsoullis G;

XX WPI; 2000-106100/09.

XX New isolated human genes and the secreted polypeptides they encode,

PT useful for diagnosis and treatment of e.g. cancers, neurological

PT disorders, immune diseases, inflammation or blood disorders -

PS Disclosure; Page 34; 586pp; English.

XX 297019 to 297137 represent 94 isolated human secreted protein genes.

CC Y86215 to Y86333 are the secreted proteins encoded by the 94 human genes.

CC This sequence represents a fragment of one of the human secreted

CC proteins. The genes and their corresponding secreted polypeptides are

CC useful for preventing, treating or ameliorating medical conditions,

CC e.g., by protein or gene therapy. Also pathological conditions can be

CC diagnosed by determining the amount of the new polypeptides in a sample

CC or by determining the presence of mutations in the new genes. Specific

CC uses are described for each of the 94 genes, based on which tissues they

CC are most highly expressed in, and include developing products for the

CC diagnosis or treatment of cancer, tumours, developmental abnormalities

CC and foetal deficiencies, blood disorders, diseases of the immune system,

CC autoimmune diseases, inflammation, allergies, Alzheimer's and cognitive

CC disorders, schizophrenia, arthritis, asthma, psoriasis, sepsis, skin

CC disorders, atherosclerosis, diabetes, cardiovascular disorders, kidney

CC disorders, digestive/endocrine disorders, infections and AIDS. The

CC polypeptides are also useful for identifying their binding partners.

CC The sequences shown in Y86334 to Y86585 represent fragments of the

CC secreted proteins.

XX SQ Sequence 17 AA:

Query Match 67.4%; Score 29; DB 21; Length 17;

Best Local Similarity 50.0%; Pred. No. 8.3;

Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IFGSLAFL 9

::|::|::|

```

Db      2 vygsmf1 9
RESULT 10
Y48923
ID      Y48923 standard; Peptide; 7 AA.
XX      AC
XX      Y48923;
DT      10-DEC-1999 (first entry)
XX      DE Membrane dipeptidase-binding ovary homing peptide #11.
XX      Homing peptide; organ; tissue; lung; pancreas; skin; retina; MDP;
KW      prostate; ovary; lymph node; adrenal gland; liver; gut; tumour;
KW      membrane dipeptidase.
XX      XX
OS      Synthetic.
OS      Homo sapiens.
XX      PN W09946284-A2.
XX      PD 16-SEP-1999.
XX      PF 10-MAR-1999; 99WO-US05284.
XX      PR 13-MAR-1998; 98US-0042107.
XX      PR 26-FEB-1999; 99US-0042107.
XX      PA (BURN-) BURNHAM INST.
XX      PI Rajotte D, Pasqualini R, Ruoslahti EI;
XX      WPI: 1999-571717/48.
XX      DR
XX      PT New peptides which selectively home to organs or tissues, used for,
XX      e.g. identifying target ligands and for therapy of pathological
XX      conditions _
XX      PS Example 6; Page 152; 193pp; English.
XX      CC The present invention describes peptides that selectively home to a
XX      tissue or organ. The peptides can be used for identifying an organ
XX      or tissue, for identifying a target molecule expressed by an organ or
XX      tissue or for treating an organ or tissue pathology, where the organ or
XX      tissue is selected from prostate, lung, skin, retina, pancreas, gut,
XX      ovary, adrenal gland, liver, and lymph node. The peptide bind to the
XX      membrane dipeptidase (MDP). Y48618 to Y49066 represent sequences
XX      which are used in the exemplification of the present invention.
XX      SQ Sequence 7 AA;
XX      Query Match 58.1%; Score 25; DB 20; Length 7;
XX      Best Local Similarity 71.4%; Pred. No. 2.1e+05;
XX      Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX      QY 3 FGSLAFL 9
XX      Db 1 fgsqafv 7
XX      RESULT 11
XX      Y84219
XX      ID Y84219 standard; peptide; 16 AA.
XX      AC Y84219;
XX      DT 03-JUL-2000 (first entry)
XX      DE Amino acid sequence of a peptide.
XX      KW Modulator; sterol-regulated Site-1 protease; cholesterol;
KW      sterol regulatory element binding protein; SREBP; lipid synthesis;
KW      fatty acid biosynthesis; site-1 protease; protease inhibitor;
KW      serum cholesterol; hypercholesterolemia; lipid metabolism.
XX      OS Synthetic.
XX      FH Key Location/Qualifiers
XX      FT Modified-site 1
XX      FT /note= "amidated residue"
XX      FT Misc-difference 16
XX      FT /note= "COOH attached"
XX      PN W0200009677-A2.
XX      PD 24-FEB-2000.
XX      PF 13-AUG-1999; 99WO-US18544.
XX      PR 14-AUG-1998; 98US-0096571.
XX      PR 23-JUL-1999; 99US-0360237.
XX      PA (TEXA ) UNIV TEXAS SYSTEM.
XX      PA (BROW/) BROWN M S.
XX      PA (CHEN/) CHENG D.
XX      PA (ESPE/) ESPENSHADE P J.
XX      PA (GOLD/) GOLDSTEIN J L.
XX      PA (RAWS/) RAWSON R B.
XX      PA (SAKA/) SAKAI J.
XX      PI Brown MS, Cheng D, Espenshade PJ, Goldstein JL, Rawson RB;
XX      PI Sakai J;
XX      DR WPI: 2000-224327/19.
XX      PT Novel assay for identifying modulators of sterol-regulated Site-1
XX      protease useful for the treatment of hypercholesterolemia, involves
XX      identifying an agent capable of down regulating Site-1 protease
XX      activity _
XX      PS Example 11; Page 106; 172pp; English.
XX      CC The specification describes a method for identifying modulators of a
XX      sterol-regulated Site-1 protease. Site-1 protease cleaves sterol
XX      regulatory element binding proteins (SREBPs) in the endoplasmic
XX      reticulum, initiating release from membranes and activating lipid
XX      synthesis. The modulators therefore also modulate cholesterol and
XX      fatty acid biosynthesis. The method comprises selecting an agent capable
XX      of down regulating Site-1 protease and formulating a composition
XX      comprising the agent. The site-1 protease inhibitors are useful for
XX      treating a patient for elevated serum cholesterol. Diseases treated
XX      include hypercholesterolemia and other lipid metabolism associated
XX      conditions. The present sequence was used in the course of the
XX      invention.
XX      SQ Sequence 16 AA;
XX      Query Match 58.1%; Score 25; DB 21; Length 16;
XX      Best Local Similarity 62.5%; Pred. No. 53;
XX      Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX      QY 1 KIFGSLAF 8
XX      Db 2 kvfrslkf 9
XX      RESULT 12
XX      Y84229
XX      ID Y84229 standard; peptide; 16 AA.
XX      AC Y84229;
XX      DT 03-JUL-2000 (first entry)

```

XX Amino acid sequence of a peptide derived from site-1 protease.
 DE Modulator; sterol-regulated Site-1 protease; cholesterol;
 XX sterol regulatory element binding protein; SREBP; lipid synthesis;
 KW fatty acid biosynthesis; site-1 protease; protease inhibitor;
 KW serum cholesterol; hypercholesterolemia; lipid metabolism.
 XX
 OS Synthetic.
 OS Crictetus sp.
 XX WO200009677-A2.
 PN
 XX
 PD 24-FEB-2000.
 XX
 XX 13-AUG-1999; 99WO-US18544.
 XX
 XX 14-AUG-1998; 98US-0096571.
 PR
 PR 23-JUL-1999; 99US-0360237.
 XX
 XX (TEXA) UNIV TEXAS SYSTEM.
 PA (BROW/) BROWN M S.
 PA (CHEN/) CHENG D.
 PA (ESPE/) ESPENSHADE P J.
 PA (GOLD/) GOLDSTEIN J L.
 PA (RAWS/) RAWSON R B.
 PA (SAKA/) SAKAI J.
 XX
 XX Brown MS, Cheng D, Espenshade PJ, Goldstein JL, Rawson RB;
 PI Sakai J;
 PI
 XX WPI; 2000-224327/19.
 DR
 XX
 XX Novel assay for identifying modulators of sterol-regulated Site-1
 PT protease useful for the treatment of hypercholesterolemia, involves
 PT identifying an agent capable of down regulating Site-1 protease
 PT activity -
 XX
 XX Disclosure; Fig 24A; 172pp; English.
 PS
 XX The specification describes a method for identifying modulators of a
 CC sterol-regulated Site-1 protease. Site-1 protease cleaves sterol
 CC regulatory element binding proteins (SREBPs) in the endoplasmic
 CC reticulum, initiating release from membranes and activating lipid
 CC synthesis. The modulators therefore also modulate cholesterol and
 CC fatty acid biosynthesis. The method comprises selecting an agent capable
 CC of down regulating Site-1 protease and formulating a composition
 CC comprising the agent. The site-1 protease inhibitors are useful for
 CC treating a patient for elevated serum cholesterol. Diseases treated
 CC include hypercholesterolemia and other lipid metabolism associated
 CC conditions. The present sequence is derived from site-1 protease,
 CC and is used in the course of the invention.
 XX
 SQ Sequence 16 AA;
 Query Match 58.1%; Score 25; DB 21; Length 16;
 Best Local Similarity 62.5%; Pred. No. 53;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 KIFGSLAF 8
 Db 2 kvfrslkf 9
 RESULT 13
 W95382
 ID W95382 standard; peptide; 18 AA.
 XX
 AC W95382;
 XX
 DT 17-MAR-1999 (first entry)
 XX

DE Antimicrobial peptide fragment from ubiquicidine (residues 1-18).
 XX Ubiquicidine; treatment; diagnosis; prophylaxis; infection; microbial;
 KW pathogenic; Gram-positive bacteria; antimicrobial; Staphylococcus aureus;
 KW Listeria monocytogenes; Gram-negative; Klebsiella pneumoniae; E. coli;
 KW enterococcus; Salmonella typhimurium; Mycobacterium avium; M. fortuitum;
 KW fungus; Candida albicans; Cryptococcus neoformans; Aspergillus fumigatus;
 XX virus; parasite; Trypanosoma cruzi; Taxoplasma gondii.
 XX Synthetic.
 OS Mus sp.
 XX WO9854314-A1.
 PN
 XX 03-DEC-1998.
 PD
 XX 29-MAY-1998; 98WO-NL00311.
 PF
 XX 29-MAY-1997; 97NL-1006164.
 PR
 XX (OYLE-) RIJKSUNIV LEIDEN.
 PA
 XX Feitsma RIJ. Hiemstra PS, Nibbering PH, Pauwels EAJ;
 PI Van Den Barselaar MT;
 PI
 XX WPI; 1999-070214/06.
 DR
 XX New antimicrobial peptides derived from ubiquicidine - useful for
 PT the prophylaxis, diagnosis and treatment of infections in humans and
 PT animals
 PT
 XX Claim 3; Page 23; 48pp; English.
 XX
 CC Sequences W95381-389 represent antimicrobial peptide fragments derived
 CC from ubiquicidine. Ubiquicidine or optionally modified peptide fragments
 CC of ubiquicidine, may be used for the treatment, diagnosis, or prophylaxis
 CC of infections in humans and animals. In particular the products and
 CC methods are directed against microbial infections caused by pathogenic
 CC Gram-positive Staphylococcus aureus, including antibiotic resistant
 CC strains, Listeria monocytogenes, and Gram-negative antibiotic resistant
 CC Klebsiella pneumoniae, E. coli, enterococci, and Salmonella typhimurium
 CC bacteria, micro-organisms difficult to treat such as Mycobacterium avium
 CC and M. fortuitum, fungi such as Candida albicans, Cryptococcus
 CC neoformans, and Aspergillus fumigatus, viruses, in particular enveloped
 CC viruses, and parasites such as Trypanosoma cruzi and Taxoplasma gondii.
 XX
 SQ Sequence 18 AA;
 Query Match 58.1%; Score 25; DB 20; Length 18;
 Best Local Similarity 71.4%; Pred. No. 60;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 KIFGSLA 7
 Db 1 kvhgsla 7
 RESULT 14
 W60420
 ID W60420 standard; peptide; 7 AA.
 XX
 AC W60420;
 XX
 DT 24-AUG-1998 (first entry)
 XX
 DE Tumour homing peptide of the invention.
 XX
 KW Tumour homing peptide; in vivo panning; murine melanoma; tumour.
 XX Synthetic.
 OS
 XX WO9810795-A2.
 PN

XX PD 19-MAR-1998.
 XX PF 10-SEP-1997; 97WO-US16086.
 XX PR 10-SEP-1996; 96US-0710067.
 XX PA (BURN-) BURNHAM INST.
 XX PI Pasqualini R, Ruoslahti E;
 XX DR WPI; 1998-207151/18.
 XX PT Tumour homing molecules and their conjugates - useful for, e.g.
 XX PT directing linked moiety to tumour containing angiogenic vasculature
 XX PS Example 5; Page 80; 105pp; English.
 XX CC W60390-432 represent peptides recovered from mouse melanomas.
 CC The peptides are tumour homing peptides, and are identified by in
 CC vivo panning. The in vivo panning comprises administering a library
 CC of diverse peptides to a subject having a tumour, collecting a sample of
 CC the tumour, identifying a peptide that homes to the tumour, collecting a
 CC sample of normal tissue corresponding to the tumour, and determining that
 CC the peptide that homes to the tumour is not present in the normal tissue.
 CC The tumour homing peptides can be linked to a moiety (e.g. doxorubicin),
 CC and used to direct the moiety to a tumour.
 XX SQ Sequence 7 AA;

Query Match 55.8%; Score 24; DB 19; Length 7;
 Best Local Similarity 83.3%; Pred. No. 2.1e+05;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GSLAFL 9
 || |||
 Db 1 gsfafl 6

RESULT 15
 W93747
 ID W93747 standard; Peptide; 7 AA.
 AC W93747;
 XX
 XX 28-JUN-1999 (first entry)
 DT
 XX
 DE Mouse B16D15b melanoma derived tumour homing peptide 32.

XX Tumour homing peptide; tumour; diagnosis; endothelial cell; melanoma;
 KW angiogenic vasculature; anti-tumour; anti-inflammatory; anti-angiogenic;
 KW anti-arthritis; NGR receptor; inhibitor; angiogenesis; anticancer drug;
 KW prognosis; inflammation; regeneration; wounded tissue; targeting;
 KW macular degeneration; diabetic retinopathy; rheumatoid arthritis;
 KW occlusive thrombus; murine.

XX Mus sp.
 XX
 XX WO9913329-A1.
 XX
 XX 18-MAR-1999.
 XX
 XX 08-SEP-1998; 98WO-US18895.
 XX
 XX 25-AUG-1998; 98US-0139802.
 XX 10-SEP-1997; 97US-0926914.
 XX
 XX (BURN-) BURNHAM INST.
 XX
 XX Pasqualini R, Ruoslahti E;
 XX WPI; 1999-215158/18.
 DR

XX Identifying molecules that home to angiogenic vasculature used as
 PT targets for anticancer agents
 XX
 XX Example VI; Page 115; 180pp; English.
 XX
 CC This invention describes novel peptides which home to angiogenic
 CC vasculature, specifically of a tumour and which have anti-tumour,
 CC anti-inflammatory, anti-angiogenic and anti-arthritis activity. Such
 CC molecules are identified by treating a purified NGR receptor with a test
 CC compound and identifying compounds that bind specifically to the NGR
 CC receptor. The peptides of the invention are inhibitors of angiogenesis
 CC and can be used to produce conjugates for delivering agents to angiogenic
 CC vasculature, particularly anticancer drugs or an imaging agent, for
 CC diagnosis or prognosis. These conjugates may be directed to non-tumour
 CC angiogenic vasculature, e.g. that present in inflammatory, regenerating
 CC or wounded tissue, e.g. for treatment of macular degeneration, diabetic
 CC retinopathy or rheumatoid arthritis. The peptides provide specific
 CC targeting to tumours, especially their supporting vasculature, since the
 CC NGR receptor is exposed to the circulation only in angiogenic
 CC vasculature. Precise targeting should reduce the systemic toxicity of
 CC anticancer drugs in the conjugates. Complete killing of all target cells
 CC may not be essential since partial denudation of endothelium may result
 CC in an occlusive thrombus, and endothelial cells are unlikely to become
 CC resistant to anticancer agents nor to lose the targeting receptor.
 CC W93622-W93809 and W93843-44 are examples of tumour homing peptides used
 CC in the invention.
 XX SQ Sequence 7 AA;

Query Match 55.8%; Score 24; DB 20; Length 7;
 Best Local Similarity 83.3%; Pred. No. 2.1e+05;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GSLAFL 9
 || |||
 Db 1 gsfafl 6

RESULT 16
 W93317
 ID W93317 standard; peptide; 11 AA.
 XX
 AC W93317;
 XX
 XX 28-MAY-1999 (first entry)
 DT
 XX
 DE r-CGRP-alpha-27-37 peptide #14.

XX CGRP; calcitonin-gene-related peptide; rCGRP-alpha; treatment; headache;
 KW non-insulin-dependent diabetes mellitus; cardiovascular disease; asthma;
 KW skin disease; inflammatory disease; allergic rhinitis; immunoassay;
 KW excessive vascular dilation; concomitant reduced tissue blood flow;
 KW morphine tolerance; antibody; diagnostic; neurotransmitter.
 XX
 OS Synthetic.

XX Key Location/Qualifiers
 FH Modified-site 11
 FT /note= "C-terminal amide"
 XX
 XX DE19732944-A1.
 XX
 XX 04-FEB-1999.
 XX
 XX 31-JUL-1997; 97DE-1032944.
 XX 31-JUL-1997; 97DE-1032944.
 XX
 XX (THOM) THOMAE GMBH KARL.
 XX Beck-Sicklinger A, Entzeroth M, Rlst B;
 PI

XX WPI; 1999-122216/11.
 XX Derivatives of calcitonin-gene-related peptide fragment - useful as
 PT diagnostic reagents and as CGRP antagonists, for treatment of
 PT cardiovascular diseases, headaches and asthma
 XX
 XX Claim 4; Page 18; 19pp; German.
 XX The invention describes peptides derived from calcitonin-gene-related
 CC peptide (rCGRP-alpha) (positions 27-37) sequence H-FVPTNVGSEAF-NH₂ where
 CC (i) 1-3 of the amino acids in the sequence FVPTNVGSE are replaced with K,
 CC Y, A, F, P, Hyp, S, L, Q, D, H, Acp, Pac, Tic, Hop, Aib, I or G; or (ii)
 CC the sequence FVPTNVGS is replaced with NFVPRSKISP, NVAPRSKISP, NVAPTNGS
 CC or ISSTNGS; and/or (iii) 1-8 of the amino acids in the sequence
 CC FVPTNVGSE are deleted and (iv) one amino acid in the sequence FVPTNVGSEAF
 CC can be a D-amino acid and (v) the N-terminal amino group can be
 CC substituted by a protecting group R selected from 3,3-diphenylpropionyl,
 CC 2-propylpentanoyl, 3,5-dichlorophenoxyacetyl, 1-adamantylacetyl,
 CC 3,5-dibromo-4-hydroxyphenylalanyl,
 CC 4-(4-benzhydryl-1-piperazinyl)-1,5-dioxo-3,3-(tetramethylene)-pentyl or
 CC 5,11-dihydro-6-oxo-6H-dibenz[b,e]azepin-11-carbonyl. The peptides are
 CC useful for treating headache, non-insulin-dependent diabetes mellitus,
 CC cardiovascular diseases, skin diseases, inflammatory diseases, allergic
 CC rhinitis, asthma, diseases involving excessive vascular dilation and
 CC concomitant reduced tissue blood flow, and morphine tolerance. They are
 CC also useful for producing and purifying antibodies, as immunoassay
 CC reagents, as diagnostic and analytical tools in neurotransmitter
 CC research.
 XX
 XX Sequence 11 AA:
 SQ
 Query Match 55.8%; Score 24; DB 20; Length 11;
 Best Local Similarity 100.0%; Pred. No. 58;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 GSLAF 8
 Db 7 gslaf 11
 RESULT 17
 Y98857
 ID Y98857 standard; Peptide; 15 AA.
 AC Y98857;
 XT 07-AUG-2000 (first entry)
 XX
 XX HLA class II binding antigen epitope peptide #46.
 XX Human leucocyte antigen; HLA class II; antigen epitope; pharmaceutical;
 KW immune response; chronic viral disease; cancer; autoimmune disease;
 KW rheumatoid arthritis; multiple sclerosis; myasthenia gravis; AIDS;
 KW allograft rejection; allergy; Lyme disease; hepatitis; prostate cancer;
 KW glomerulonephritis; food hypersensitivity; malaria.
 XX Unidentified.
 OS
 XX W09961916-A1.
 PN
 XX 02-DEC-1999.
 PD
 XX 28-MAY-1999; 99WO-US12066.
 PF
 XX 29-MAY-1998; 98US-0087192.
 PR
 XX (EPIM-) EPIMUNE INC.
 PA
 XX Sette A, Southwood S, Sidney J;
 PI
 XX WPI; 2000-097143/08.
 DR

XX New compositions containing immunogenic peptide epitopes for various
 PT HLA class II DR molecules useful for inducing helper T cell response -
 XX
 XX Claim 1; Page 40; 60pp; English.
 XX
 XX The present invention relates to a new pharmaceutical composition
 CC comprising a unit dose form of a peptide, or analogue, comprising an
 CC epitope selected from those represented by peptides Y9812-Y9939 which
 CC are derived from various antigens for various human leucocyte antigen
 CC class DR molecules, representative of the world wide population. The
 CC peptide/analogue binds to an HLA class II molecule at an IC-50 of less
 CC than or equal to 1,000 nM. The pharmaceutical can be used to induce a
 CC helper T cell response. The pharmaceutical focuses the immune response
 CC towards selected determinants and could therefore be used in cases of
 CC chronic viral diseases and cancer. Examples of diseases that can be
 CC treated using the peptide containing pharmaceutical include autoimmune
 CC diseases (rheumatoid arthritis, multiple sclerosis, and myasthenia
 CC gravis), allograft rejection, allergies, Lyme disease, hepatitis, and
 CC post-streptococcal endocarditis or glomerulonephritis and food
 CC hypersensitivities. The peptide epitopes can be used to enhance immune
 CC responses against other immunogens administered with the peptides.
 CC Diseases which can be treated using immunogenic mixtures include prostate
 CC cancer, hepatitis B, hepatitis C, AIDS, renal carcinoma, cervical
 CC carcinoma, lymphoma, and condyloma acuminatum. The peptides may also be
 CC used to make monoclonal antibodies useful as potential diagnostic or
 CC therapeutic agents. The peptides may also be useful as diagnostic
 CC reagents, for example, to determine the susceptibility of an individual
 CC to a treatment regimen. Also, the peptides may be used to predict which
 CC individuals will be at substantial risk of developing chronic infection.
 CC The selection of appropriate T and B cell epitopes should allow the
 CC development of epitope based vaccines particularly towards conserved
 CC epitopes of pathogens which are characterized by high sequence
 CC variability such as HIV, HCV and Malaria.
 XX
 XX Sequence 15 AA:
 SQ
 Query Match 55.8%; Score 24; DB 21; Length 15;
 Best Local Similarity 62.5%; Pred. No. 80;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 KIFGSLAF 8
 Db 8 kvlgsgaf 15
 RESULT 18
 R64603
 ID R64603 standard; Peptide; 16 AA.
 AC R64603;
 XX
 XX 01-SEP-1995 (first entry)
 DT
 XX RF-1 peptide 48 from respiratory syncytial virus.
 DE
 XX antiviral activity; DP-178; DP-107; diagnostic; HIV-ILAT;
 KW human immunodeficiency virus; transmembrane protein; gp11;
 KW alpha helix; leucine zipper; DP-185; respiratory syncytial virus;
 KW RSV.
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FH Modified-site 1 /note= "optionally has an amino, acetyl,
 FT 9-fluorenylmethoxy-carbonyl, hydrophobic or
 FT macromolecular carrier gp. attached"
 FT Modified-site 16 /note= "optionally has a carboxyl, amido, hydrophobic
 FT or macromolecular carrier gp. attached"
 FT
 XX

PN W09428920-A.
 XX 22-DEC-1994.
 XX 07-JUN-1994; 94WO-US05739.
 XX 07-JUN-1993; 93US-0073028.
 XX (UYDU-) UNIV DUKE.
 XX Barney SO, Bolognesi DP, Lambert DM, Matthews TJ;
 PI Petteway SR, Wild CT;
 XX WPI: 1995-036105/05.
 XX Computer search generated synthetic peptides - are inhibitors of
 PT HIV transmission
 XX Claim 14; Page 138; 182pp; English.
 XX R64591-623 are peptide derivatives of a 37 mer RF-1 peptide derived
 CC from respiratory syncytial virus (RSV) (R64590) which have been
 CC truncated at the amino terminus. The peptides are DP-178 like
 CC peptides. DP-178 corresponds to amino acids 638 to 673 of the HIV-1
 CC isolate LAI transmembrane protein gp41. It forms a putative alpha
 CC helix at the C-terminal end of the gp41 ectodomain, and complexes
 CC with DP-107 (corresponds to amino acids 558-595) which contains a
 CC leucine zipper motif. The peptides complex via non-covalent
 CC protein-protein interactions. The peptide derivatives were
 CC identified by a computer assisted peptide sequence search. The
 CC antiviral activity of this peptide is not stated in the
 CC specification.
 XX Sequence 16 AA;
 SQ

 Query Match 55.8%; Score 24; DB 16; Length 16;
 Best Local Similarity 66.7%; Pred. No. 85;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

 QY 1 KIFGSLAFL 9
 II IIII;
 Db 1 kingslafl 9

 RESULT 19
 R64604
 ID R64604 standard; Peptide; 17 AA.
 XX R64604;
 AC
 DT 01-SEP-1995 (first entry)
 XX RF-1 peptide 49 from respiratory syncytial virus.
 DE
 DE
 XX antiviral activity; DP-178; DP-107; diagnostic; HIV-1LAI;
 KW human immunodeficiency virus; transmembrane protein; gp41;
 KW alpha helix; leucine zipper; DP-185; respiratory syncytial virus;
 KW RSV.
 XX Synthetic.
 OS
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "optionally has an amino, acetyl,
 FT 9-fluorenylmethoxy-carbonyl, hydrophobic or
 FT macromolecular carrier gp. attached"
 FT Modified-site 17
 FT /note= "optionally has a carboxyl, amido, hydrophobic
 FT or macromolecular carrier gp. attached"
 XX
 PN W09428920-A.
 XX

PD 22-DEC-1994.
 XX 07-JUN-1994; 94WO-US05739.
 XX 07-JUN-1993; 93US-0073028.
 XX (UYDU-) UNIV DUKE.
 XX Barney SO, Bolognesi DP, Lambert DM, Matthews TJ;
 PI Petteway SR, Wild CT;
 XX WPI: 1995-036105/05.
 XX Computer search generated synthetic peptides - are inhibitors of
 PT HIV transmission
 XX Claim 14; Page 138; 182pp; English.
 XX R64591-623 are peptide derivatives of a 37 mer RF-1 peptide derived
 CC from respiratory syncytial virus (RSV) (R64590) which have been
 CC truncated at the amino terminus. The peptides are DP-178 like
 CC peptides. DP-178 corresponds to amino acids 638 to 673 of the HIV-1
 CC isolate LAI transmembrane protein gp41. It forms a putative alpha
 CC helix at the C-terminal end of the gp41 ectodomain, and complexes
 CC with DP-107 (corresponds to amino acids 558-595) which contains a
 CC leucine zipper motif. The peptides complex via non-covalent
 CC protein-protein interactions. The peptide derivatives were
 CC identified by a computer assisted peptide sequence search. The
 CC antiviral activity of this peptide is not stated in the
 CC specification.
 XX Sequence 17 AA;
 SQ

Query Match 55.8%; Score 24; DB 16; Length 17;
 Best Local Similarity 66.7%; Pred. No. 91;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

 QY 1 KIFGSLAFL 9
 II IIII;
 Db 2 kingslafl 10

 RESULT 20
 P30110
 ID P30110 standard; Protein; 18 AA.
 XX P30110;
 AC
 DT 03-APR-1992 (first entry)
 XX Sequence of VP1 capsid protein residues 141-160 from the amino-
 DE terminus, FMDV, Tubingen type 0, subtype 1, strain Kaufbeuren.
 DE Antigen; Picornavirus; capsid protein; antibody; detection;
 KW vaccine; diagnosis.
 XX OS Foot and mouth disease virus.
 XX W08303547-A.
 PN
 XX 27-OCT-1983.
 PD
 XX 14-APR-1983; 83WO-0002644.
 PF
 XX 25-MAR-1983; 83US-0478847.
 PR 14-APR-1982; 82US-0368308.
 PR 20-SEP-1984; 84US-0653475.
 PR 18-DEC-1984; 84US-0682819.
 XX (BITT/) BITTLE J L.
 PA (Scri-) SCRIPPS CLINIC & RE.
 XX

PI Bittle JL, Lerner RA;

XX WPI; 1983-807942/44.

XX Antigenic peptide(s) corresp. to picornavirus capsid protein -

XX useful in prodn. of vaccines and in diagnostic tests

XX Disclosure: Page 14; 90pp; English.

XX The peptides of the invention corresp. to a region on the antigenic
CC Picornavirus capsid protein. The capsid protein FMDV VP1 or polio
CC virus VP1, when linked to carriers the peptides are immunogenic.
CC Dose is 20 ug-2mg peptide for inoculations.

XX Sequence 18 AA:

Query Match 55.8%; Score 24; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 96;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 FGSIA 7

Db 7 fgsia 11

RESULT 21

R64605
ID R64605 standard; Peptide; 18 AA.

XX AC R64605;

XX 01-SEP-1995 (first entry)

XX RF-1 peptide 50 from respiratory syncytial virus.

XX antiviral activity; DP-178; DP-107; diagnostic; HIV-1LAI;
KW human immunodeficiency virus; transmembrane protein; gp41;
KW alpha helix; leucine zipper; DP-185; respiratory syncytial virus;
KW RSV.

XX Synthetic.

XX Key Modified-site 1 Location/Qualifiers

FT /note= "optionally has an amino, acetyl,
FT 9-fluorenylmethoxy-carbonyl, hydrophobic or
FT macromolecular carrier gp. attached"

FT Modified-site 18 /note= "optionally has a carboxyl, amido, hydrophobic
FT or macromolecular carrier gp. attached"

XX WO9428920-A.

XX 22-DEC-1994.

XX 07-JUN-1994; 94WO-US05739.

XX 07-JUN-1993; 93US-0073028.

XX (UYDU-) UNIV DUKE.

XX Barney SO, Bolognesi DP, Lambert DM, Matthews TJ;

XX Petteway SR, Wild CT;

XX WPI; 1995-036105/05.

XX Computer search generated synthetic peptides - are inhibitors of
XX HIV transmission
XX Claim 14; Page 138; 182pp; English.
XX R64591-623 are peptide derivatives of a 37 mer RF-1 peptide derived

CC from respiratory syncytial virus (RSV) (R64590) which have been
CC truncated at the amino terminus. The peptides are DP-178 like
CC peptides. DP-178 corresponds to amino acids 638 to 673 of the HIV-1
CC isolate LAI transmembrane protein gp41. It forms a putative alpha
CC helix at the C-terminal end of the gp41 ectodomain, and complexes
CC with DP-107 (corresponds to amino acids 558-595) which contains a
CC leucine zipper motif. The peptides complex via non-covalent
CC protein-protein interactions. The peptide derivatives were
CC identified by a computer assisted peptide sequence search. The
CC antiviral activity of this peptide is not stated in the
CC specification.

XX Sequence 18 AA:

Query Match 55.8%; Score 24; DB 16; Length 18;

Best Local Similarity 66.7%; Pred. No. 96;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KIFGSLAFL 9

Db 3 Kingqlafi 11

RESULT 22

R64606
ID R64606 standard; Peptide; 19 AA.

XX AC R64606;

XX 01-SEP-1995 (first entry)

XX RF-1 peptide 51 from respiratory syncytial virus.

XX antiviral activity; DP-178; DP-107; diagnostic; HIV-1LAI;
KW human immunodeficiency virus; transmembrane protein; gp41;
KW alpha helix; leucine zipper; DP-185; respiratory syncytial virus;
KW RSV.

XX Synthetic.

XX Key Modified-site 1 Location/Qualifiers

FT /note= "optionally has an amino, acetyl,
FT 9-fluorenylmethoxy-carbonyl, hydrophobic or
FT macromolecular carrier gp. attached"

FT Modified-site 19 /note= "optionally has a carboxyl, amido, hydrophobic
FT or macromolecular carrier gp. attached"

XX WO9428920-A.

XX 22-DEC-1994.

XX 07-JUN-1994; 94WO-US05739.

XX 07-JUN-1993; 93US-0073028.

XX (UYDU-) UNIV DUKE.

XX Barney SO, Bolognesi DP, Lambert DM, Matthews TJ;

XX Petteway SR, Wild CT;

XX WPI; 1995-036105/05.

XX Computer search generated synthetic peptides - are inhibitors of
XX HIV transmission
XX Claim 14; Page 138; 182pp; English.
XX R64591-623 are peptide derivatives of a 37 mer RF-1 peptide derived
XX from respiratory syncytial virus (RSV) (R64590) which have been
XX truncated at the amino terminus. The peptides are DP-178 like

CC peptides. DP-178 corresponds to amino acids 638 to 673 of the HIV-1
 CC isolate LAI transmembrane protein gp41. It forms a putative alpha
 CC helix at the C-terminal end of the gp41 ectodomain, and complexes
 CC with DP-107 (corresponds to amino acids 558-595) which contains a
 CC leucine zipper motif. The peptides complex via non-covalent
 CC protein-protein interactions. The peptide derivatives were
 CC identified by a computer assisted peptide sequence search. The
 CC antiviral activity of this peptide is not stated in the
 CC specification.
 XX
 SQ Sequence 19 AA;

Query Match 55.8%; Score 24; DB 16; Length 19;
 Best Local Similarity 66.7%; Pred. No. 1e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KIFGSLAFL 9
 || |||||
 Db 4 kingslafi 12

RESULT 23
 ID Y89178 standard; peptide; 19 AA.
 XX
 AC Y89178;
 DT
 XX 23-MAY-2000 (first entry)
 DE Core polypeptide fragment T No. 617.
 XX
 KW Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
 KW HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
 KW anti-fusogenic; differentiation factor; interleukin; interferon;
 KW colony stimulating factor; hormone; angiogenic factor.
 XX
 OS Unidentified.
 XX
 PN WO959615-A1.
 XX
 PD 25-NOV-1999.
 XX
 PF 20-MAY-1999; 99WO-US11219.
 XX
 PR 20-MAY-1998; 98US-0082279.
 XX
 PA (TRIM-) TRIMERIS INC.
 XX
 PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DW;
 XX
 DR WPI: 2000-136792/12.
 XX
 PT A new hybrid polypeptide with enhanced pharmacokinetic properties
 XX comprises enhancer sequence -
 XX
 PS Disclosure; Page 31; 124pp; English.
 XX
 CC The invention relates to hybrid polypeptides comprising enhancer peptide
 CC sequence linked to core polypeptides. The enhancer polypeptides are
 CC derived from various retroviral envelope (gp41) protein sequences,
 CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
 CC pharmacokinetic properties such as increasing the half-life of any core
 CC polypeptide that they are linked to. The core polypeptides are any
 CC polypeptide that may be introduced into a living system and that can
 CC function as a pharmacologically useful peptide for the treatment or
 CC prevention of a disease. The core polypeptides are bioactive peptides
 CC selected from a growth factor, cytokine, differentiation factor,
 CC interleukin, interferon, colony stimulating factor, hormone or angiogenic
 CC factor. The peptides of the invention can be used for inhibiting viral
 CC infection and can be used in anti-viral and anti-fusogenic treatments.
 CC Sequences Y88651-Y90055 represent core polypeptide fragments that can be
 CC used in the invention. Some sequences among those indicated also comprise

CC enhancer fragments at terminal ends and form hybrid polypeptides.
 XX
 SQ Sequence 19 AA;

Query Match 55.8%; Score 24; DB 21; Length 19;
 Best Local Similarity 66.7%; Pred. No. 1e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KIFGSLAFL 9
 || |||||
 Db 11 kingslafi 19

RESULT 24
 ID R64607 standard; Peptide; 20 AA.
 XX
 AC R64607;
 DT
 XX 01-SEP-1995 (first entry)
 DE RF-1 peptide 52 from respiratory syncytial virus.
 XX
 KW antiviral activity; DP-178; DP-107; diagnostic; HIV-1LAI;
 KW human immunodeficiency virus; transmembrane protein; gp41;
 KW alpha helix; leucine zipper; DP-185; respiratory syncytial virus;
 KW RSV.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /note= "optionally has an amino, acetyl,
 FT 9-fluorenylmethoxy-carbonyl, hydrophobic or
 FT macromolecular carrier gp. attached"
 FT Modified-site 20 /note= "optionally has a carboxyl, amido, hydrophobic
 FT or macromolecular carrier gp. attached"
 XX
 PN WO9428920-A.
 XX
 PD 22-DEC-1994.
 XX
 PF 07-JUN-1994; 94WO-US05739.
 XX
 PR 07-JUN-1993; 93US-0073028.
 XX
 PA (UYDU-) UNIV DUKE.
 XX
 PI Barney SO, Bolognesi DP, Lambert DM, Matthews TJ;
 PI Petteway SR, Wild CT;
 XX
 DR WPI: 1995-036105/05.
 XX
 PT Computer search generated synthetic peptides - are inhibitors of
 XX HIV transmission
 XX
 PS Claim 14; Page 138; 182pp; English.
 XX
 CC R64591-623 are peptide derivatives of a 37 mer RF-1 peptide derived
 CC from respiratory syncytial virus (RSV) (R64590) which have been
 CC truncated at the amino terminus. The peptides are DP-178 like
 CC peptides. DP-178 corresponds to amino acids 638 to 673 of the HIV-1
 CC isolate LAI transmembrane protein gp41. It forms a putative alpha
 CC helix at the C-terminal end of the gp41 ectodomain, and complexes
 CC with DP-107 (corresponds to amino acids 558-595) which contains a
 CC leucine zipper motif. The peptides complex via non-covalent
 CC protein-protein interactions. The peptide derivatives were
 CC identified by a computer assisted peptide sequence search. The
 CC antiviral activity of this peptide is not stated in the
 CC specification.
 XX

SQ Sequence 20 AA; 55.8%; Score 24; DB 16; Length 20;
Query Match Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 KIFGSLAPL 9
|| ||||
Db 5 Kingdslafi 13

RESULT 25

Y82864
ID Y82864 standard; peptide; 9 AA.

XX AC Y82864;

XX DT 19-JUN-2000 (first entry)

XX DE Uroplakin tumour associated antigen (TAA).

XX KW Tumour associated antigen peptide; TAA; cancer; carcinoma;
KW treatment; prevention; cure; anti-tumour vaccine; metastases;
KW breast; bladder; prostate; pancreas; ovary; thyroid; colon;
KW stomach; carcinoma; MHC Class I; HLA-A2; human;
KW Major Histocompatibility Complex; uroplakin;
KW prostate specific antigen; prostate specific membrane antigen;
KW prostate acid phosphatase; mucin; lactadherin;
KW teratocarcinoma derived growth factor; PSA; PSMA; PAP; CRIPTO-1.

XX OS Homo sapiens.

XX PN WO200006723-A1.

XX PD 10-FEB-2000.

XX PF 29-JUL-1999; 99WO-IL00417.

XX PR 30-JUL-1998; 98IL-0125608.

XX PA (YEDA) YEDA RES & DEV CO LTD.
XX (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX PI Eisenbach L, Carmon L, Tirosh B, Bar-haim E, Paz A, Fridkin M;
XX Filtzer-attas C;

XX DR WPT; 2000-205463/18.

XX PS Claim 4; Page 104; 113pp; English.
XX
CC Tumour associated antigen peptides (TAA) may be used for the
CC treatment, prevention and cure of cancer or cancer metastases. The
CC cancer may be breast, bladder, prostate, pancreas, ovary, thyroid,
CC colon, stomach, head or neck cancer or a carcinoma. The tumour
CC associated antigens are presentable to the immune system by HLA-A2
CC molecules and are generally between 8 to 10 amino acids in length.
CC The amino acids located at positions 2 and 9 of the tumour associated
CC antigens are the anchor residues which participate in the binding to
CC MHC class I molecules, more specifically HLA-A2. More tumour
CC associated antigens are described in GENESEQ records Y82806-Y82882.
CC Those tumour associated antigens described in records Y82806-Y82824
CC and Y82855-Y82869 are derived from Uroplakin, such as Uroplakin II,
CC Uroplakin Ia, Uroplakin III and Uroplakin Ib. Those described in
CC records Y82825-Y82829 are derived from prostate specific antigen
CC (PSA). Those described in records Y82830-Y82835 are derived from
CC prostate specific membrane antigen (PSMA). Those described in
CC records Y82836-Y82839 are derived from prostate acid phosphatase
CC (PAP). Those described in records Y82840-Y82846 are derived

